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Best Local Similarity 100.0%;
Matches 2565; Conservative
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                                                                      the invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polypophides (AAM78.23-AAM8242) that exhibit antivit, clather to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypophides are useful in gene therapy, vaccines or populate therapy. The polypophides are useful in gene therapy, vaccines or populate therapy. The polypophides have various cytokine like activities, e.d. stem cell growth testor the tity, hapmangelesis regulating activity a figure architecture are interested in the diagnosts and/or treatment of cancer, loopeania, persons system disorders, arthritis and
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                                    Note: Records for SEC ID NO 2119 (AAES2591), 2111 (AAES2592) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
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                          The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foctal liver. The single exon nucleic acid probes may be used for predicting.
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total liver. The present sequence is a single exon nucleic acid
               measuring and displaying gene expression in samples derived from human
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                                                                                     Claim 1; SEO ID NO 8964; 639pp + sequence listing; English
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ttp.wipo.int/pub/published_pct_sequences.
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microarray: Alzheimer's disease; multiple selerosis: schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2273 taaaaqqaaqaeeeetttqaaqqtaffqqaaqaatqqaaqaetcaeetcafeeeefetet 2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2213 geagatygatgaettagagggagetgeteeteetatteeeeeeaggeteeacteegagga 2272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 563 BP; 145 A; 120 C; 141 G; 157 T; 0 other;
                                                                                                                                                                                                                                                                                                                    09-A06-2001
                                                                                                                                                                                                                                                                                                                                                 WO200157275 A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruman brain expressed single exon probe SEQ ID No: 8982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-NoV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK08941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK08941 Standard: DNA; 563 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2333 graetytyetyyayytyaacagaaagaggaatet 2366
                                                                                                                                                                                                                                                                                                                                                                                                        epilepsy: cameer; ss.
                             brains -
                                                                       WPT: 2001-483446/52.
                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                    30 JAN-2001; 2001WO US00667
                                           Single exon nucleic acid probes for analyzing gene expression in buman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                514 geaetgtgetggaggtgaaeagaaagaggtetgt 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        454 taabaqqabqaeeeetttqabqqtattqqbbqabqabqqbbetebeetetetet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 3.9%;
Similarity 98.5%;
                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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2000GB-0024263.
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Pred. No. 4.5e-56;
                                                                                                       Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 563;
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Example 4, SEQ ID NO: 8932; 650pp + Sequence Listing: English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Greek Match
Rost Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FER 2000; 2000US-0180312
25-MAY-2000; 2000US-0207456
40-JUN 2000; 2000US-0508408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homony bose marrow expressed extra processions as microsarray; cancer; leakaemia; lymphema; myeloma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1007 - VIOL
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Buman genome-derived simple each note in a 13 pt besome C.1
                                                                                     WPI: 2001-488900/51.
                                                                                                                                                                                                                                         (MOLE)
                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000; 2000US-0234687
27-SEP-2000; 2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                     U3-ADG-2000; 2000US-0632366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN 2001; 2001WO US00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NoV-2001 (tirst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK34832 standard; DNA; 563 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eptilepsy and cancers. The present sequence is one of the probes of the
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Local Similarity 98.5%;
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                                                                                                                                                                                                                                         MOLECULAR DYNAMICS INC
                                                                                                                                                               Hanzel DK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservation
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20000UB-0024263.
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                                                                                                                                                                   Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proceedings in analysis, protection
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                                                                                                04 FEB 2000; 2000US-0180412.
26-MAY-2000; 2000US-0068408.
30-JUN-2000; 2000US-0632466.
21-SEP-2000; 2000US-06324647.
21-SEP-2000; 2000US-0244647.
27-SEP-2000; 2000US-0244649.
04-0CT-2000; 2000GB-0024264.
WELL 2001 4888 17,753.
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                             Penn SG,
                                                                                                                                                                                                                                                                              09-AUG-2001.
                                                                                                                                                                                                                                                                                                              W0200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                  qenetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                 Probe; microarray, human, placenta, antenatal diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                 Prodes #9235 used to Scasure Actor expression in human placenta sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI40549 standard; DNA; 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing dene expression in homan bone marrow
                                                                  (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probes which are derived from denomic sequences expressed in the human
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                             Chen W,
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: Pred. No. 4.5e-56;
0: Mismatches 4
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                               Rank DR;
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Best Local Similarity 98.5
Matches 270; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes (SENF). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                          11 Nov 1994;
                                                                                                                                                                                                                                                                            W09514772 Al
                                                                                                                                                                                                                                                                                                                                                                                                                Human dene sidnature HUMGS04364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA122707 standard; cDNA to mRNA; 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID No 9235; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Jenome derived single exon nucleic acid probes useful for
tor diagnosis of abnormal cell function, by preparing cDNA that
                                                                                                                                                                                                                                           01 JUN 1995
                                                                                                                                                                                                                                                                                                                                               cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                               human; cloning; mapping; non-biased library; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                               Gene signature; messenger RNA; mkNA; relative abundance; frequency;
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                                                  WP1; 1995 206931/27.
                                                                                      Marsabara K, Okubo K;
                                                                                                                     (CKUBZ) CKUBO K.
                Identifying gene signatures in \beta'-directed human cDNA library - e.g.
                                                                                                                                       (MATS/) MATSUBARA K.
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                                                                                                                                                                        93.712 0355504
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                                                                                                                                                               29 JUL-1999;
27-AUG-1999;
11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 From various human tissues, synthesis of china was initiated from the from various human tissues, synthesis of china was initiated from the frequency of a stated solution of the frequency of the frequency of the frequency of the frequency of a different menas. Each library is constructed so as to reflect accurately the relative abundance of different menas in the particular lissue from which it was derived. The appearance frequency of a diven GS in a clina library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function of tor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1195; 2245pp; Japanese.
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Pred. No. 7.8e 46;
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I. Wakamatsu A. Nagai E.
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Human; nootropic; neuroprotective; cytostatic; dermatological; cirucide; immunosuppressive; antiinlammatory; anti-HUV; antibactorial; voluciary; antiparkinsonian; antisiskling, antianment; antiarthritic; cancer; anticheumatic; heparictropic; ocrebropretective; antiinlammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifundal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
neurological disease; infection; nephrotropic; gene therapy: vaccine;
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                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at htp.wipo.int/pub/published_pet_sequences.
                                                                                                                  (d) would healing: (e) neurological diseases e.g. carebral anexia and epilepsy; and (t) infectious diseases such as viral, bacterial, fundal and parasitic infections.
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                                                                                                                                                                                                                                                                                                                                                                          protein or gene therapy. The genes are isolated from a range of man tissues disclosed in the specification. The machine acids, proteins antibodies and (ant)agonists are useful in the diagnosis, treatment and
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                                             : The sequence data for this patent did not form part of the ted specification, but was obtained in electronic format dire WIFO at IIp.wipo.int/pub/published_pet_sequences.
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Best Local Similarity 81.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the PRO polypeptides may modulate glucose or tree fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A peptide
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## SUMMARIES

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## ALIGNMENTS

MEDITINE REFERENCE ACCESSION VERSION KEYWORDS SOURCE AF222980 REFERENCE DEFINITION RESULT ORGANISM TITLE AUTHORS JOURNAL TITLE AUTHORS 2 (bases 1 to 6930) Millar, K., Anderson 1 (bases 1 to 6930)
Millar, J.K., Wilson-Annan, J.C., Anderson, S., Christie, S.,
Millar, J.K., Wilson-Annan, J.C., Anderson, S., Christie, S.,
Taylor, M.S., Semple, C.A., Beyon, R.S., Clair, D.M., Mull, W.J.,
Blackwood, D.H. and Porteous, D.J.
Disruption of two nevel genes by a translocation co-sequenting with schizophrenia Homo sapiens Eukaryota: Metazoa: Chordata: Craniata: Veriebrata: Putologstomi: Mammalia: Eutheria: Primates: Catarrhini, Hominidae: Homo. Hum. Mol. Genet. 9 (9), 1415-1423 (2000) , 20275630 AC222980 6930 bp mRNA linear FWI 02 JUN Homo sapiens disrupted in Schizophrenia 1 protein (DISCI) mENNA. Direct Submission complete cds. AF222980.1 GI:8163868 human. ., Anderson, s. and Christie, S. PRI 62 JUN 2000

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Homo Sapiens mRNA for KIAA0457 protein, partial eds.
AB007926.1 GI:3413875
KIAA0457 protein.
Homo sapiens
                                                                Submitted (08-001-1997) Osamu Obara, Kazusa DNA Research Institute,
Laboratory of DNA Technology: Yana 1532 G. Kisarazu, Chiba
292-0812, Japan (E-mail:ednainfo@kazusa.or.jp, Tel:081-4-08-52-0013,
Fax:081-4-08-52-3914)
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from human brain
           Characterization of cDNA clones in size fractionated cDNA libraries
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Nakajima, U., Nomura, N. and Obara, O.
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2994	GATTCTATAAAAAGGAAACCAAGCATAAGACTCTGTCATCATACCTGTTACACGGTTCCTA	2935	qq
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2954	gatttqaqaataqtttcatctcaqcccccattaqaqaqaaqttqqqqtqaattctqqaa	2895	Ç,
2814	CCTTCTAAA IGTCACTCAAAAAATTTCTTTTTCCATGTCATTCTTGGGAATGTCTTCCACAG	2755	del
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4874 4794	af agott fatot ogagoagatacagototagatatttaataataagtataattagott 	481 473
7 8	qqetqqqqt eeaqqaaacaaaqeaaaaqeacaatatqtgaatqtqctgattqtttccc 	475 467
4754 4674	reatyetqtyeageaettetqteeteugteaaggagatygceatgettaageeageaat	469 461
4694 4614	tdteafttertdaadteaeaetddrdf tceadaaddeatetgdtgcttfgcteage 	463 455
יט סרי		457 449
س حتب	taeeacaqat qqtaaatttaateeaqtqqttqt tetgtttqtqettetgttetcattt 	451 443
n 4	Lt taear cacht tagaaaceacact cacacttt tgeagagtgttgagcttaataacta 	445
حه نت	ceatagatet agtat igt aeageactgeattetetgaggaagteecagteecagteetetellililililililililililililililili	431
4394 4314	refraaarttteraagtilaatggategtgaattttttteatgtaactectatte 	4.25
4334 4254	CATTAGCATAILAGICTGAGACAGAGAGAGAGAGAGAGAGCTCACTTAGAGTLIAGCGAGAGCTCACTTAGAGTTTAGCGCATTAGAGTTAGAGTTAGAGTTAGAGTAGAGAGCTCACTTGAGTTTAGCGCAGAGCTCACTTGAGTTAGGAGAGCTCACTTGAGTTAGGAGAGCTCACTTGAGTTAGGAGAGCTCACTTGAGTTAGGAGAGAGA	427
→ t.)	qqf ennqf aeet f.qq.baataeaeecataeecataatafetget tqqaqaaeescatatge 	421 413
4214 4134	auauturantyauyaayytypeersayayaayntetetaaanaaggagtacootete 	415 407
C -	uctaydactectattgagaeagetucaaaacaggetgatttcaattaggeagcaette 	4015
0	qtsycayfaet eat aaf geaag geaf f eagget eetgaggtgggt tetttggggg 	403
4034 3954	t dat beit engt act at bagt beitgagt bet that bat beggebat git begt bebeggt bebeg 	4.84
	det tauf daedeagfigtagtigefeagtaggaeugeatagtaeteagfaacaeuggge 	181
	oct cadt apreset gerat get et cadt apreset tele tele treet tersteret aggegatigas 	385 377
	act caylastacayt acaytactcaytaayycaytatgytactcaytaaagcaatgo	37'9 371
3714	$s_{-G} \texttt{TACTCAGTAACAGTGCAGTACTCAGTAAGGCAGTACTCAGTAACACAGAGTGCAGT}$	465

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282	eageeteesaagtagetggggttacaggesttgeseggesetgatgattttgtat	5815	Qy
		5895	Db
185	quenegeaateteqqeteaetqeaaeetetaeeteeeaqqtteaaqetattetaetqeet	5835	Qy
584		5755	Db
583	adattteattttttttttttqaqatqqaqteetetetetete	5775	Qy Dh
577	ttcactqgcctqaqttaqqacatqctatcaqtaataqtcccaqttccatcca	5715	Qy
569		5635	Db
571	gtgatattatactqtctqccttqctqqaatqctqqctttcaaatqqtcacccattiitci	5655	Ωy
563		5575	
565	Catactggaaatgalqaqtlaqaatetqatttgactgggatqttttalqaqaatqtaaqt	5595	Оу
		5515	Db
554	catcaaaacaacaacaatqaaatttatgttqqcqataqccacaaaccacaagcaaaaqca	5535	Qy
551		5455	Db
554	gcaqtttttqtcaqqqqaacalaaaaatatccaaqaqaqqtlaqqqcttaqaatttaaaaq	5475	Qy
545		5395	Db
547	gtottaagongotttgacoolqqqaqacacagqactgtgtatoolcaatcatactataca	5415	Оу
539		5335	
533	agloogetaagggecagegtgettettetggetaeacaaectteteaggaeaageeeact	5355	Qy
		5275	Db
527	Lt.aaccacaagccataactcatctgttgttctttgcttgqtcttagaqtatcattcagaaaalliiii	5295 5215	Οy
529 521	t agalantgigilt calt tooctgolgoaaat titgaaglat titgggoaggigat tagilit is sa titgggoaggigtigat tagilit is sa titggaaglat titgggoaggigaggigat tagilit is sa titggaaglantnigggoaggigaggigaigaigaiga nagaaglantnigggoaggigaggigaigaigaigaigaigaigaigaigaigaig	5155	Ф
515	caagttaataactgccttgaattgtttgaacccgaaataaqggttctttgqtacctctaa	5175	Qy
		5095	Db
517	tattaeteagaeseeatealgaaslaattetgtyäggteatgatgtatttgaaaattetg	5035	Оу
509			Db
g 503	tetttteaaaaageeteeeagaeaeaagaeatettaaeegtegetageeeaagtgttttq	5055	Qу
		4975	Db
505	aactiggiaaqagtcaggattggccacattgccaataacaaattcctacttcqacatatq	4995	Qy
497		4915	Db
499	aqaaaattatqaactqqtcacatqqcacttqqaatccttqaqttaattccaqtqaaqcaa	4935	Qy
491		4855	Db
493	875 tleetggaetteaittleaalgalgaaceaaatleetgaattattialaaligtgtetaa 491	4875	Qy
485		4795	Db

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AL445200
AL445200.1 GT:10718452
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arbitrary. Caps between the contids are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            egin 1sA, ux. Esmail enquiries: humquerysander.ac.uk elone
requests: elonerequestasander.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enkaryota: Metažoa: Chordata: Craniata: Vertebrata: Enteleostomi:
Mammalia: Entheria: Primates: Catarrhini: Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 131554; sum-of-contigs
Insert size: 149216; 5.4% error; agarose Ip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: dJ852F22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Sander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molay, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEBBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coverage: 3.12x in Q20 bases; agarose tp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 3.44x in Q20 bases; sum of contids Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencind vector: plasmid; L08752; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4; version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: humquery sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NoTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    consists of 16 conties. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 133054)
                                                                                                                                                                                                                                                       114594 114693; dap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11345 11444; dap of 100 bp
11445 15274; contiq of 3840 bp in length
                                                                                                                                                                                                                                                                                                                                92707 96333; con
96334 96433; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80927 81026; gap of 100 bp
81027 89376; contig of 8350 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78279 78378; gap of 1
78379 80926; contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46479 46578: gap of 100 bp
46579 61624: contig of 15046 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                      92607 92706; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B9477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89477 89476; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70569
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18431 38813: contid of 20383 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15275 15374: dap of 100 bp
15375 18330: contiq of 2956 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70469 70568:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6859-6958: gap of 100 bp
6959 11344: contig of 4386 bp in length
            /db_xret "taxon:9606"
/chromosome "l"
                                                                                         /organism "Homo sapiens"
                                                                                                                                                                          tocation/qualitiers
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                                                                                                                                             . 133054
                                                                                                                                                                                                                          133054; contiq of 18361 bp in
                                                                                                                                                                                                                                                                                                  114593; contid of 18160 by in length
                                                                                                                                                                                                                                                                                                                                                                               96333; contid of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46478; contig of 3387 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42991:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Summary Statistics
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100 bp

2548 bp in length

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misc_feature
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fragment_chain:1"
46579    .61624
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ACCESSION
VERSION
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                                                                                                                     DEFINITION
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                                                                       AL353052 151132 bp DNA Homo sapiens chromosome 1 clone RP5-865N13, PROGRESS ***, 11 unordered pieces.
           AL353052
AL353052 CI-9800738
                                                                                                             . *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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* consists of 11 contigs. The true order of the pieces 
* is not hown and their order in this sequence record is 
* arbitrary. Gaps between the contigs are represented as 
* runs of N. but the exact sizes of the pages are unknown. 
* This record will be updated with the finished sequence 
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 150132; sum-of-contigs
Insert size: 139673; 9.2% error; agarose-fp
Quality coverage: 3.79% in Q20 bases; sum of contigs Quality
coverage: 4.26% in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus quality: 144541 bases at least Q40 Consensus quality: 146975 bases at least Q30 Consensus quality: 148633 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CR10 15A, UK. E mail enquiries: humquery@sanger.ac.ak Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: dJ865N13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: SC
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Mammalia: Butheria: Primates: Catarrhini; Hominidae: Homo.
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9221 193573; contig of 11373 bp in length
103574 103673; gap of 100 bp
103674 109214; contig of 5541 bp in length
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23162 41268: contia of 18207 bp in length

41364 41468: gap of 100 bp

41469 68843: contia of 27375 bp in length
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114281: contig of 4967 bp in length
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92120: costig of 23177 bp in length
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2 (bases I to 1874)
Sugano, S., Suzaki, Y.,
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                      construction, 5': & 3' end one pass sequencing: Department of Vitology and Human Genome Center, Institute of Medical Science,
                                                                                   NEW human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert
                                                                                                                                                  Laboratory of Genome Structure Analysis, Human Genome Center;
Shirokane dai, 4-6-1, Minato-kn, Tokyo 108-8639, Japan
(E-mail:edual@ims.u-tokyo.ac.)p, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                   Shibabara, T., Tanaka, T. and Nakamura, Y
                                                                                                                                                                                                                                                                                                                                                                                                                 Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., okamoto,S., okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
  University of Tokyo (partly supported by Science and Technology
                                                                   sequencing: Research Association for Biotechnology; cDNA library
                                                                                                                                     Fax:81 3 5449 5416)
                                                                                                                                                                                                                 Sugano, Institute of Medical Science, University of Tokyo
                                                                                                                                                                                                                                          Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
                                                                                                                                                                                                                                                                                                                                                                       NEDO human cDNA sequencing project
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                                                                                                                       teleteageeetteagtelettggetaeaegggtetetgeagaettggeeeaggeegeaa 897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >> 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                          IMPORTANT: This sequence is not the entire insert of clone RPIL-9801 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RPIL-9801 is at 1 in this sequence. The true left end of clone RPIL-9801 is at 1 in this sequence.
                                                                                                                                                                                                                                                                                                       Pieter de Jong. For further details see http: [www.el.el. and language has her let VECTOR: pBACe3.6]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery:Sanger.ac.uk Clone requests. clonerequest&sanger.ac.uk on Feb 1, 2002 this sequence version replaced gi:18250465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human DNA sequence from clone RF11 9801 on chromosome 1, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL359543
                                                                                                                                                                                                                                                                                                                                                                                                                                            Group. Further intormation can be found at http://www.samper.ic.ak/BBS/Chrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.satoper.ac.uk/Prejects/T_elegans/Wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assembly was confirmed by restriction digest. The following abbreviations are used to associate primary acrossion numbers given in the leature table with their source databases. Em., EMBL, Sw., SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP: Information on the WORMPEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  During sequence assembly data is compared from overlapping clones Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
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Mammalia; Eutheria; Primates; Catarrhini: Hominidae; Home
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                                                                                                    The true right end of clone RP11-1784 is at 37904 in this sequence
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∕organism-"Homo sapions"
                                                                    Location/Qualifiers
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Denn,A.L., Ding,Y., Dinh,H.H., Douthwalte,K.J., Draper,H.,
Dugan Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
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Coyle,M.D., bathorne,S.R., David,R., Davila,M.L., Davis,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muzny, b.M.
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Mammalla; Eutheria; Rodentia; Schurognathi; Muridae, Murinae;
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Oniles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,L., Rolle,M.,
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
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Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
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                                                                                                        Submitted (17 SEP 2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, one Baylor Plaza, Houston, TX 77040, USA on Dec 20, 2001 this sequence version replaced di:15627717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
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Jackson, L.E., Jacobson, R., Jia, Y., Johnson, R., Jolivet, S.,
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                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C
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Center: Baylor College of Medicine
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                                                          Genome Center
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dap of unknown

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52351 52351

53498 53598

55429; contiq of 1832 bp in length 55529; gap of unknown length

gap of unknown

length

contig of 1508 bp in length gap of unknown length contig of 1147 bp in length

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* consists of 51 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hqse.bem.tmc.edu/docs/Nenbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* NOTE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * arbitrary, Caps between the contids are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality coverage: 0x in 020 bases; agarose to estimation quality coverage: 1.1x in 020 bases; sum of configs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hdsv.ben.tum/.cdu/
Contact: huse-help@bem.tmc.edu
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contid of 1463 bp in length
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contid of 1933 bp in length
             gap of unknown
                                contig of 1170 bp in length
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                                                                                              contig of 1531 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Thomas Hudson
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                                                                                                                                                                                                                                                                                                                                                                                                                               110 .
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Total Vol: 20 ul
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Primer: each 5 pM
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PCR Cycles: 35
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24. .48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Ems. EMBL. Sw. Sw. Sw. Sept. 1 to TREMBL. Wp., WORMPEP: Information on the WormMPEP database can be found at http://www.sameper.ac.uk/Projects/C electris/wormpep. This sequence was generated from part of bacterial cloue contigs of human chromosome 1, constructed by the Samper Centre Chromosome 1 Mapping Group. Further information can be found at Engl. 2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           requests: clonerequest sanger actual on Nov 8, 2000 this sequence version replaced di:10715861.

During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemistry or covered by high quality data (i.e., phred quality do); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MIA subclone; and the assembly was contirmed by restriction digest. RPA 740BIA is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16 MAK-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coville, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is the entire insert of clone RP4 700H3 This sequence was finished as follows unless otherwise noted: all regions were either double stranded or sequenced with an alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 100170)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the library RPCL 4 constructed by the group of Pieter de Jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sij∕www. chori ora/barpar/home.htm
                                                                               complement(join(+147. .255,17641. .17905,67802.
/gene "bisel"
/note "match: cDNAs: Em:AF222980 Em:AB007926
match: proteins: Tr:075045"
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/deme="ptsett"
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/chromosome="]"
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/product "dJ7308i3.1 (disrupted in schizophrenia I)"
                                /evidence_not_experimental
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Query Match 3.9%; Score 267.6; DB 9; Length 100176; Best Local Similarity 98.5%; Pred. No. 3.3e-58;
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22825...23588
/more "LIM4 repeat, matches 2101...2925 of consensus."
23655...25145
                                                                                                                                              /mote-"AluSi repeat: matches 1. .311 of consensus" 41652. .41792
/mote "MIE repeat. matches 7. .166 of consensus" 41864. .42129
                                                                                                                                                                                                                                                                                                                                                   /note-"match: GSS: Em:AQ683363"
39501...39917
/note-"hatch: GSS: Em:AQ088544"
complement(49885...40383)
/gone-"pisci"
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26792...2688]

2note-*10 copies 9 mer tqttittqt 71% conserved"
26799...26878

26704...40 copies 2 mer tt 63% conserved"
27364...27547

27364...11MD repeat: matches -17...167 of consensus"
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29epe "DISCI"
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Zhate mil MD repeat metches 474
26792. 26881 has 6 mor idittitut
                                                                 /mote-"MIE repeat: matches 32. .211 of consensus" 42877. .43020
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//docker_MIR represt, matches 59. .233 of consensus"
41234. .41326
//note "MiR repeat, matches 166. .252 of consensus"
41326. .41651
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                                                                                                         42614.
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/uote="MLT1G repeat: matches l. .261 of consensus"
32979, .37095
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28092, .28203
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36753, .36960
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25800. .26697
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25313. [2561]
                                                                                                                            /note-"L/ repeat: matches 24v8. .2688 of consensus"
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84127. .34397
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Zhotë "HALT repeat: matches 626. 1730 it consensus"
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 CMCTGCAAGTETCCACTGCTTGGGAAAGTGTGGGAAGCTGGAACTTGGAAACTTGTCGATT. 17849

Matches 270;

Conservative

0; Mismatches

4; Indels 0; Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2333 geachgrachgaaggraacagaaaggaaret 2366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALA45200 Linear RTG 10 JUL-2001 Homo sapiens chromosome I cione RP5-852F22, *** SEQUENCING IN PROTRESS ***, Is unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                  Consensus quality: 124266 bases at least Q40 Consensus quality: 127653 bases at least Q40 Consensus quality: 127647 bases at least Q20 Insert size: 141544, sum of contias Insert size: 145246; 5.4% error: adarose 1p quality coverade: 3.44% in Q20 bases; sum of contias Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09 JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG: HTGS PHASEL: HTGS_CANCELLED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mortay, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enkaryola; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Mammalia; Entheria; Primates; Catarrhini; Hominidae; Homo.
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consists of 16 contiqs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary, tags between the confliqs are represented as
runs of N, but the exact sizes of the gaps are unknown.

                                                                                                                                                                                                                                                                                                                                                                                     coverage: 3.12x in 020 bases; agarose tp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: dd852F22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: humquery (sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.sander.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission

this record will be updated with the finished sequence
as soon as it is available and the accession number will

                                                                                                                                                                                                                                                                                                                                               * Norm: This is a 'working draft' sequence.

    be preserved.

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            15375 18330: contiq of 2956 bp in length
18331 18430: gap of 100 bp
18431 48814: confid of 20383 bp in length
                                                                                         11345 11444: gap of 100 bp
11445 15274: confid of 3830 bp in length
                                                                          15275 15374: gap of
                                                                                                                                6859 6958; gap of 100 bp
6959 11844; contid of 4886 bp in length
38814 38913; gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Centre
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                                                                                                                                                                                 6858; contiq of 6858 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61625 61724: qap of 100 bp
61725 70468: contiq of 8744 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92607 92706; gap of 100 bp
92707 96484; contiq of 3627 bp in length
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iragment_chain:1"
15375...18330
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/chromosome "l"
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fraqment_chain:3"
92707 96333
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tragment chain:2"
70569. 78278
/note "assembly tragment:00949
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61725. .70468
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1. .6858
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tragment_chain:1"
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      fragment_chain:4"
96434. .114593
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tragment_chain:3"
                                                                                                                                                                                           81027
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tragment_chain:1"
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traument_chain:!"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                878: gap of ______100 bp ...
80926: contiq of 2548 bp in length
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    CABLIGGAAGIGCCACTGCIIGRAAAAGTGTGGGAAGCTGACTGAAACTTGTCGAIT
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    CABLIGGAAGIGCCACTGCIIGRAAAAGTGTGGGAAGCTGACTIGGAAACTTGTCGAIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome 1 clone RP11-455E8, *** SEQUENCING IN FROMRESS ***, 45 unordered pieces.
AL445284
                         Insert size: 138658; sum-of-contigs
Insert size: 249449; 25.8% error: agarese-fp
Quality coverse: 2.24x in 222 bases; sum-of-contigs quality
                                                                                                                Assembly program: XGAP4; version 4.5 sequencing vector: plasmid: L08752; 100% of reads Chemistry: Dye forminator Big Dye; 100% of reads Consensus quality: 119820 bases at least Q40 Consensus quality: 129280 bases at least Q30 Corsensus quality: 129280 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries: humquery-sanger.ac.uk clone requests: clonerequest-sanger.ac.uk un Jun 26, 2001 this sequence version replaced qi:10800735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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coverage: 1.84x in Q20 bases; agarose-tp
                                                                                                                                                                                                                                                                                                                                     Center project name: bA355E8
                                                                                                                                                                                                                                                                                                                                                               Contact: humquery/sander.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-sunger.a-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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114694. .13x054
/note "assembly_trayment:00882
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                                                                                                                                                                                                                                                                                                           Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38961 t 1502 others
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* This record will be updated with the timished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 45 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved.
                                                                                                                                                                            21900 21999; qap of
22000 25200; cont
25701 25800; 290 of
25701 25800; 390 of
25801 31546; cont
31547 31646; gap of
     126222 191093; cont
131094 131193; dap of
131194 135966; cont
                        121018 126.221; gap of 126222 126221; gap of 126222 121093; cont
                                                                                                                                                                                                                                                                                               100431 100530; gap of 100531 102587; cont
                                                                                         118134 118233: gap of 118234 120917: contiq of 120918 121017; wap of
                                                                                                                                                                                                                                                                                                                                                                             82455 85804: conces 100 bp
85804 85903: gap of 100 bp in length
95904 89932. contig of 4029 bp in length
                                                                                                                                                     115958
                                                                                                                                                                115858 115957; qap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          82355 82454:
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62330 68031; contid of 5702 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57592 57691; dap of 100 mp
57692 62229; contid of 4538 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.85 50784: dap of 100 pp 50785 54425: contid of 2641 bp in length
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47602 50684: contia of 3083 bp in leadth
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41971 43978; centin of 2008 bp in length
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34953 41870; contid of 6918 bp in length
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16727 21899: coptiq of 5173 bp in length
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2476 2475; dap of 100 bp in length
8176 8275; dap of 100 bp
8276 16626; contig of 8351 bp in length
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100430: contig of 3543 bp in length
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85803: contig of 3349 bp in length
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75837; wontig of 2621 bp in length
947; dap of 100 bp
79704; contig of 2767 bp in length
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52: contin of 3206 bp in length 100 bp
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                                        ap of 100 bp
contig of 4872 bp
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contiq of 2057 bp in length
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tragment chain:1"
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traquent_chain:1"
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/note "assembly tragment:00501
tragment_chain:6"
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fragment chain:{"
53526, 57591
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fragment_chain:2"
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tragment_chain:1"
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tragment chain:1"
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tragment_chain:6"
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tragment chain:5"
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tragment_chain:5"
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traqment_chain:4"
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/note "assembly_tragment:00054"
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138660; contid of 2594 bp in length
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Matches 254; Conservative
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality).
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG
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Human DNA sequence from clone RPI1:555L24 on chromosome L, complete
                                                                                                     corresponding to the overlapping clone, as we submit sequences with
                                                                                                                          together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                        During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations
                                                                                                                                                                                                                  on Feb 15, 2001 this sequence version replaced di:12748826.
                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                   Williams, S.
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Mammalia: Eutheria: Primates; Catarrhini: Hominidae; Homo.
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30); an attempt was made to resolve all sequencing problems,
                                                                                     only a small overlap as described above
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/note "assembly_fragment:00135"
96888. 100430
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/note: "assembly_fragment:00090"
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110252. .112417
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115998; .11813
/note "assembly_tragment:00941"
118244; .120917
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112518. .115857
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102688. .110151
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100531. .102587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.7%; Score 254; DB 2; Longth 14205B;
100.0%; Pred. No. 1.4e-54;
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FEATURES nother\_redion notion\_tedion 30 III 03 repeat\_region repeat\_region repeat region repeat\_region repeat\_region repeat, region Topost\_region norbest\_teaton misc\_feature repeat\_region neither Trodes noinen\_teaden repeat\_region repeat region repeat\_region one plasmid subclone or more than one Missubclane; and the useembly was continued by restriction didest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases. En., EMBL, 5%., notion. sections only ence, except for a 100 base overlap.

The true left end of clone RF41-5251.24 is at 1 in this sequence. The true left end of clone RF41-584N17 is at 66109 in this sequence. The true right end of clone RF11-9801 is at 56214 in this sequence. Local loc/Ocalifiers ocup: \*\*\* - 15 ti eta, i i par, bene bin VECT-R: pBACe3.6 http://www.sinact.a/.k//re/yets/Pikars,Wormpop This sequence was demorated from part of bacterial clone configs of human chromosome 1, constructed by the Sander Centre Chromosome 1 Mapping RP11-5551.24 It may be shorter because we sequence overlapping http://www.siget.ar.ok/ETE/Shil
RPI1-555024 is tram the library RPCI-11.2 constructed by the droup
of Pieter de Jong. For further details see Stoup. Further information can be tound at IMPORTANT: database can be found at SWISSPROF; Tr: 7note "27 con 8702. 58.86 /note "Tandom repeat Porced join, Gap size to be approximately 100bp by restriction digest data."  $8449,\ ...9196$ /note 7664. /not e 4207 . /moto-"MIR repeat: matches 52. .137 of consensus" 12787. .12791 Anote "Tandem repeat. Single clone region. Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly 3155 /note "Alub repeat: matches 1, .289 of consensus"
11469, .11607 /note-"LLMD2 repeat: matches 5724, .5831 of consensus" Zolomo "PP11-555L24" /note "L2 repeat: matches 2646. .2701 of consensus" Zecto "12 report: matches 2561. .2710 of consensus" /note:"MIK repeat: matches 8. .253 of consensus" 11177. .11469 /note "174 copies 2 mer 4g 53% conserved" /note "180 copies 3 mer tag 73% conserved" Contained the property of the country /orqubism "Homo sapiens" /dh\_kret "\*ar c.4606" 1. .66208 This sequence is not the entire insert of clone "".LIMO1 repeat. matches 7822. .7973 of Vonsensus" . .13497 "MIR repeat: matches 24 - 92 of consensus" "LIPA16 repeats matches 6021. .6157 of consensus" "ITEA4 repeat, matches 5584, .6144 of cossesses" "MIR repeat: matches 1. .180 of consensus" "FRAM repeat: mutches 1 155 of consensus" "MDR466 request matches 97 484 of consensus" TREMBL: Wp:, WORMPEP: Information on the WORMPEP 9888 127 mg/les 2 mer la 74% (observed) 110719 15 "RPCI 11.2" ropies 3 mer tad 79% conserved™ Restriction digest data confirm the assembly." 496 of charges

repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region televat\_region repeat\_region ropeat\_regio: repeat\_region 22288. .22583 /note "LIMASA repeat, matches 5942, .6176 of compensus" 21116, .21515 /hote/ 37421 /note "12 repeat, matches 1219, 1193 of consensus" 30566, 30693 /mote "MSIA repeat: motehes 1, .426 of consensus" 27953, .29576 26777 /note "LIM2 repeat: matches 499. . 304 of consensus" 25932. .26093 /note "AluJb repeat: matches l. .294 of consensus" 22584. .24]eH 71578 21578 /note "LIMA5A repeat, matches 6176, .6285 of consensus" 20572, .20874 /note "FIANG" repeat: matches l. .128 of consensus" 17979, .18268 /more "MER45R repeat: matches 1. .246 of consensus" 17180. .17591 /note-"MLTIAl repeat: matches 5. .465 of consensus" 15956. .16319 /mote "LiM64 repeat: matches 7167. .7852 of consensus" 14096. .14487 /hote "Alude repeat, matches 5, 1805 of consensus" 13498. 14089 /note-"Aludo repeat: matches 1, .271 of consensus" 38510, .38724 /note "112 copies 2 mer tt 74% conserved" 37717. .38003 /note "LTR160 repeat: matches 282. .487 of consensus" 34760. .35069 33338...33425 Zhote "LTR162 repeat. matches 98...188 of consensus" 33528...33633 /note "1.2 repeat: matches 2599, .2750 of consensus" 31870, .31917 30694. 31415 /note "L2 repeat. matches 1533. .2272 of consensus" 31670. .31813 /mote-"MSTA internal repeat, matches 1, .165) of consensus" 29577, .29990 /mote-"MIR repeat. matches 2. .141 of conscisus" 27529. .27952 Zuoto "LIMBS repeat: matches 5759. (618) of consensus" 27264. (2747) 18564 /note-"LIMC4 repeat. matches 6616. .7017 of consensus" 15244. .15581 /note "MIR repeat. matches 20, .235 of consensus" 39174. .39264 /mote "24 copies 2 mer da 100% conserved" 33338, .33425 /hote-"AluSq repeat. Matches l. .304 of consensus" /note "MIR repeat: matches 60, .262 of consensis" 20463, .20571 /mote "L2 repost: matches 2629. .2710 of consonans" /note "FLAM\_C repeat: matches 1. .128 of consensus" /note-"MSTA repeat: matches 1, .426 of consensus" /bote "MERSE repeat: matches L. 178 of consensus" /note "LIMA: Znote "L2 repeat: matches 1970. .2407 of consensus" "Aludo repeato matches 1, 1293 of consensus", 197275 "MSTE repeat matches i. .420 of consensus" . .22287 27455 LIMA's repeat: matches 3548. [5186 of consensus", 24427 , 30565 . 18762 repeat, matches 2591, .2718 of consensus" teperat matches 1 306 temperatus "suspension to great large large large

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DEFINITION
                                                                                                                                                                                                                                                REFERENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvediens clone CH280 49N19, *** SEQUENCING IN PROGRESS ***, 72 unordered pieces.
                                 Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Hanks, T., Barbaria, J., Benion, J., Bimage, K., Blankenburg, K., Bounin, D., Bouck, J., Bows, M., Brown, M., Bryant, M.P., Bubay, C., Burch, P., Bubay, C., Burch, P., Butay, C., Butay,
                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegious
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Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R
                                                                                                                                                                                                  Muzny, D.M., Adams, C., Adio oduola, B., Ali-osman, F.R.,
                                                                                                                                                                                                                                                                                      Raffus.
                                                                                                                                                                                                                                                                                                                        Mammalia; Entheria; Rodentia; Scinrognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                (bases 1 to 166129)
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100.0%; Pred. No. 1.5e-51;
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Hollins, B., Homsi, F., Howard, S., Buber, J., Hulykos, Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karisson, E., Keliy, S., Khan, G., King, L., Korwis, L., Kerwar, C., Krateve, T., Krosshi, A., Landry, M., Loal, B., Lowis, L.-C., Lawis, L., Li, J., Li, Z., Lichtarde, O., Licu, C., Lin, J., Liu, W., Loulseqed, H., Lozado, R.J., Lu, X., Lincher, A., Lanctet, K., Lund, K., Loulseqed, H., Lozado, R.J., Lu, X., Lincher, A., Lanctet, K., Lund, K., Loulseqed, H., Lozado, R.J., Lu, X., Lincher, A., Lanctet, K., Lund, K., Lucker, A., Lanctet, K., Lund, K., Lucker, A., Lucker, A., Lanctet, K., Lund, K., Lucker, A., Lucker, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stone.H., Sutton.A., Syatek.A., Tabor.P., Tamerisa.A., Tamerisa.K. lang.H., Tansey.J., Taylor.C., Faylor.T., Telfrod.H., Ibomas.N., Thomas.S., Usmani.K., Vasquez.D., Vera.V., Villacior.D., Vinson.K., Wall.R., Wang.S., Ward-Moore.S., Warren.K., Washington.C., Watlindton.S., Williams.G., Williamson.A., Wleezyk.K., Weeden.S., Worley.K., Wa.C., Wu.Y., Wu.Y.F., Zhou.J., Zorrilla.S., Nelson.D.
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NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                          Consensus quality: 127821 bases at least 040 (consensus quality: 13725 bases at least 040 (consensus quality: 13725 bases at least 020 (consensus quality: 144239 bases at least 020 Estimated base); 144239 bases; adatose [p estimation quality coverage: 0x in 020 bases; adatose [p estimation]
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Contact: huse-help-bem.tmc.edu
                                                                                                                                                                           quality coverage: 2.1x in Q20 bases; sum-of contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: Phrap: version 0.990329First call to
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Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
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arbitrary, Gaps between the contids are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence

    (see http://www.hiseliomiter.od/Sock/Sochaskidialt_data.html)
    NotE: This is a 'working draft' sequence. It currently

                                                                                                                                                                                                                                    consists of 72 conties. The true order of the pieces is not known and their order in this sequence record is
                                       be preserved.
                                                                              as soon as it is available and the accession number will
8883; contid of 8883 bp in length
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8884

15930; contid of 6947 bp in length

8983; gap of unknown length

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACO22220 2333 bp DNA linear HTG 17
Homo sapiens chromosome X clone RP11 815F17, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus quality: 228469 bases at least Q40 consensus quality: 229857 bases at least Q40 consensus quality: 240504 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemistry: Dye primer ET; 66% of reads
Chemistry: Dye-terminator Hig Dye; 44% of reads
Assembly program: Phiap; version 0.990319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: H_NHO815F17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
2 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 214000; agarose tp
Insert size: 23359; sum of configs
Quality coverage: 7.60 in 020 bases; agarose-tp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: MI3: 66% Sequencing vector: plasmid: 34%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center Center Code: WHGSC
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on Aug 17, 200
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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consists of 10 contiqs. The true order of the pieces
is not known and their order in this sequence record is

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality coverage: 6.98 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web_site:http://genome.wustl.edu/qse/index.shtml
                                                                                                                                                                                                                                                                                                                                     * arbitrary. Gaps between the contids are represented as * runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NoTE: This is a 'working draft' sequence. It currently

    be preserved.

                                                                                                                                                                                                                                                                                        * This record will be updated with the finished sequence
                                                                                                                                                                                                                                      as soon as it is available and the accession number will
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11219
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1324: gap of unknown length
11218: config of 9894 bp in length
11318: gap of unknown length
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FEATURES
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                                                                                                                                                                                                                                                                                                  35172 TOATATOTITAGGICAATTICTTTICTTTTTTTTTTTTTTTTTTTAAAACCAAGTCTGGGTCT (524)
                                                                                                                                                 85232 GTCACCCAGGCTGGAATGCAGTGG --CAAGATCTCGGCTCACTGCAACCTCCACCTCCC 35288
                                                                           35349 CCACGTCCGGCTGATTTTGTATTTTTAATAGAGACAGGCTTTCACCATGTTGGCCAGAC 35408
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47444, .63537
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/note:"assembly_name:Contiq36
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11419, .20516
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92060. .127450
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/chromosome "X"
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127450: contig of 35391 bp in length
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182595: contig of 55045 bp in length
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20616: dap of unknown length
34259: contid of 13643 bp in length
44359: dap of unknown length
47343: contid of 12984 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91959; contig of 28322 bp in length
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Post processing: Minimum Match 0%
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Issued_Patents_NA:*

1: /wqq22_6/prodata/2/lima/5A_COMB.seq:*

2: /cqu2_6/prodata/2/lima/5H_COMB.seq:*

3: /cqu2_6/prodata/2/lima/6H_COMB.seq:*

4: /cqu2_6/ptodata/2/lima/6H_COMB.seq:*

5. /cqu2_6/ptodata/2/lima/6H_COMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

## SUMMARIES

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                                                                                     US OB 367 B41A 43
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Patent No. 6419687
             Concry Match (10%) Score 206.2; DB 4; Length 22481; Hest Local Similarity 79.8%; Pred. No. 5.1e 42;
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AFFLICANT: Chadri, Gorald J.; Rodriquez,
AFFLICANT: Iquacio R.; Mazzruk, Krzysztof:
AFFLICANT: Tombran Fink, Joyce
Matches 269;
                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
INFORMATION FOR SEO ID NO: 43:
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CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
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                                                    INFORMATION FOR SEQ ID NO:
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APPLICANT: Patricia; Schwartz, John P.;
APPLICANT: Taniwaki, Takayuki
FITLE OF INVENTION: PIGMENT EPITHELIUM
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APPLICATION NUMBER: 08/257,963
FILLING DATE: 07-JUN-1994
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COMPUTER: Floppy Disk
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FILING DATE: 30-DEC-1994
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TYPE: Nucleic Acid
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               22481 Base Pairs
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DERIVED FACTOR: CHARACTERIZATION GENOMIC
ORGANIZATION AND SEQUENCE OF THE PEDF GENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 32, Application 08,709018584A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schomm, James W.
APPLICANT: Bacher, Jettery W.
LITLE OF INVENTION: IDENTIFYING AND METHOD FOR
LITTLE OF INVENTION: IDENTIFYING AND ANALYZING INTERMEDIATE FANDEM
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REFERENCE, TOWKET MUMBER: 16
                                                                                                                            APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: REPEAT DNA MARKERS
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                                                                                                                                                                                                                       Diskette - 3.5 inch, 1.44 Mb
                                                                                                         04-Feb-1998
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US-09-318-448 5
, Sequence 5, Application US/99318448
; Patent No. 6210950
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US-09-018-584A-32
                                                                                                                          US-09-318-448-5
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Johnson, William G.

APPLICANT: Stentoos, Edward S.

TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND INFAILNG
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
                                                                                                                                                                                                                       : SOFFWARE: Patentin Ver. 2.0 : SEQ ID NO 5
Ouery Match 3.0%; Score 204.6; DB 4; Length 7720; Best Local Similarity 79.0%; Pred. No. 6.9e-42; Matches 282; Conservative 0; Mismatches 69; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 268; Conservative
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                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: GS/03/318,448
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TELEPAX: (608) 257-2275
INFORMATION FOR SEU ID NO: 42
                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
                                                                                                                                            TYPE: DNA ORGANISM: Homo supieus
                                                                                                                                                                                             LENGTH: 7720
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POSITION IN GENOME:
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STRANDEDNESS: Double
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          Ouery Match
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                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHERENT APPLICATION DATA:
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                                                                                                                                                                        MOLECULE TYPE: DNA (denomic)
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                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC
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                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/687,080
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                                                                                              INDIVIDUAL ISOLATE:
                                                                                                                                                                                                 : Atmitted of
                                                                                                                                                                                                                                                        LENGTH: 1386 base pairs
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350 Cambridge Avenue, Suite 250
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                                                                                                                                                                                                                                                                                                               E (415) 324 D8BO
(415) 324-0960
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IBM PC compatible
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N: 435
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Score 204.2; DB 2; Length 1386;
Pred. No. 3.2e-42;
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                                                                                                                                                                                                                                                                                                                                                                                               US-09-797-906-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                               Matches 275;
                                                                                                                                                                                                                                                                                                                        Query Match 2.9%; Score 200; DH 4; Length 84495; Best Local Similarity 76.0%; Pred. No. 4.2e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-03-05 NUMBER OF SEQ 10 NOS: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/797,906
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                                                                                                                                                                                                                                      20196 AAFTECCE EFFETETETETETETETAGACACAACICTCACCACCACAACACAACACAA 20187
                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: n - A,T,C or G
                                20136 GTGCAGTGG ---TGCGATCTCAGCTCACTACAACCTCCTGCTCCCAGGTTCAAGCGATTC 20080
                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 84495
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                                                                                                                                                                                                                                                                                                               Conservative
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58-09-508-285A-59
: Sequence 50, Application 75/00608285A
: Farent No. 63-50)3
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APPLICANT:
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comMuttek: HRM 8° compatible
oPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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THILE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
NUMBER OF SEQUENCES: 8
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                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                       CLASSIFICATION:
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REGISTRATION NUMBER: 36,816
                                                                                                                                                                                                                                                                                                              FIGURE DATE: 07 OCT 1993
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                                                                               Greer, Helen
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; Patent No. 5789223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
opPPATING SYSTEM: PC-DES/MS DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TELEPHONE: 617-720-3500
TELEPAX: 617-720-2441
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APPLICANT: Stambolian, Dwight
TITLE OF INVENTION: Hyman Galactokinase Gene
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TELECOMMUNICATION INFORMATION:
                                                                               FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                               PRIOR APPLICATION DATA:
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TYPE: nucleic acid
STRANDEDNESS: single
             REFERENCE/IDOCKET NUMBER: P50
                                         NAME: Eagle, Alissa M. REGISTRATION NUMBER:
                                                                                                                                                                       CLASSIFICATION: 436
                                                                                                                                                                                           FILING DATE:
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US-08-451-778A-7
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GENERAL INFORMATION:
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8-45]-777A-7
APPLICATION NUMBER: POT/US94/10825
FILING DATE: 23-SEP-1994
ALTORNEY/AFENT INFORMATION:
NAME: Edulo, Alissu M.
REGISTRATION NUMBER: 37,126
                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 23-SEP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig. 1. For accordance to an experimental properties and the transfer and the transfer accordance of the second sectors of the second 
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Focal Similarity 82.98; Pred. No. 2.1e-40;
Res. 252: Conservative O; Mismutches 47; Indels 5; Caps
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                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE, Falcolls B-Lease #1.0, Version #1.40
CURRENT APPLICATION DATA:
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                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08,74
FILING DATE: 26-MAY-1995
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APPLICANT: Stambolian, Dwi
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                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Human Galactokinase Gene
                                                                                                                                                                                                                                                                                                                           ARCHELSEL. SWITEFIFE Be dam 2-16./20rporate
ADDRESSE: Intellectual Property
STREET. 700 Swedeland Road/DW2220
CITY: King of Prussia
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                                                                             CLASSIFICATION: 435
                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                         STATE:
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    APPLICATION NUMBER
                                                                                                                        ABBRICATION NUMBER -
                                                                                                                                                                                                                                                                     Z1P:
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                                                                                                                                                                                                                                                                   19406-0939
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PCT/05344/10825
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ATTORNEY/AGENT INFORMATION: NAME: Eaglis, Alissa M.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7. Application PCTBS9506744 GENERAL INFORMATION:
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Hest Local Similarity 82.9%: Prod. No. 2.1e 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPAX: 610 270 5090 7:
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TELEPHONE: 610-270-5364
                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6077 FOR ATC. TRACEPORCEROACTECCAAAAGTGCTGGGATTACAGGTGTGAGCACCGCCCA 6055
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PRIOR APPLICATION DATA:
                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRECTONDENCE ADDRESS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Human Galactokinase Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bergsma, Derk J. APPLICANT: Stambolian, Dwight
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OPERATING SYSIEM: PC bosyms bos
                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Kind of Blussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: 709 Swedeland Road/HW2220
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                                                                                            FILING DATE
                                                                                                                                APPLICATION NUMBER: PCT/US95/06743
                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
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, Sequence 11, Application US/08960022
; Patent No. 5976847
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                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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FILING DATE: 23-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                          APPLICANT: Lavallie, Edwar
APPLICANT: Racio, Lisa A.
APPLICANT: Merberg, bavid
APPLICANT: Treacy, Mantice
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallie, Edward R.
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                                                                                                                                                                            TITLE OF INVENTION: SECRETED PROTEINS AND POLYNOCLEOTIDES TITLE OF INVENTION: ENCODING THEM NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6056 CCCA 6059
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                     COMPUTER READABLE FORM:
                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       APPLICANT: Spaniding, Vikki
APPLICANT: Agostino, Michael J.
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                                                                                          STREET: 87 Campr
CTTY: Cambridge
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                                                          COUNTRY:
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy disk
                                          2117:
                                                                                                                                        ADDRESSEE:
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                                                                                                                 E: Genetics Institute, Inc
E7 CambridgePark Drive
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                                                          U.S.A.
                                                                                                                                                                                                                                                                               Treacy, Maurice
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Jeffrey A.
34,028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 498-8284
TELEPAX: (617) 876-5851
INFORMALLON FOR SEU ID NO: 11:
                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDERMESS: double
                                                                                                                                 MOLECULE TYPE: CDNA
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                                                                       1593 GIBAGPTACCCTGCCTGGCCTACCTT 1528
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OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIA Release #1.0, Version #1.30

JURKENI APPLICATION DAIA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
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Copyright (c) 1993 2000 Comp
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## ALIGNMENTS

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RESULT AB007926 REFERENCE REFERENCE SOURCE KEYWORDS VERSION ACCESSION DEFINITION Locus TITLE JOURNAL ORGANISM TITLE AUTHORS AUTHORS AB007926 6833 bp mRNA linear PRI 13-AUG-1 Homo sagiens mRNA for KIAA0457 protein, partial (ds. AB007926 I GI:3413875 KIAA0457 protein. KIAA0457 protein. Homo sagiens male brain cDNA to mRNA, clone\_lib.p8loescriptli SK price\_Brone\_HG0643. Direct Submission
Submitted (08-007-1997) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
292 0912, Japan (E mail:cdmainfockacusa.or.jp, Tel:+81 438 52-3914) 2 (sites) Seki,N., Ohira,M., Nagase,T., Ishikawa,K., Miyajima,N., Nakajima,D., Nomura,N. and Ohara,O. Characterization of cDNA clones in size-fractionated cDNA libraries Ohara, O. Eukaryota: Metamoa; Chordata; Craniata; Vertebrata; Euteleostemi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. L. (bases 1 to 6833) Homo sapiens PRI 13-AUG-1998

Resuit.

Score Match Length DB

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Description

and is derived by analysis of the total score distribution.

SUMMARIES

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                                       Millar,K., Anderson,S. and Christie,S.
Direct Submission
Submitted (11 JAN 2000) Medical Genetics Section, The University of
                                                                                                                                                                                                                                                                                                                                                                                                                    Millar.J.K., Wilson Annan,J.C., Anderson,S., Christie,S.,
Taylor.M.S., Semple,C.A., Devon,R.S., Clair,D.M., Muir,W.J.,
Blackwood,D.H. and Porteous,D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens disrupted in Schizophrenia 1 protein (DISC1) mRNA,
Edinburgh, Crewe Road, Edinburgh EH4 2XU, Scotland
                                                                                                                                                                                                                                20275630
                                                                                                                                                                                                                                                                            Hum. Mol. Genet. 9 (9), 1415-1423 (2000)
                                                                                                                                                                                                                                                                                                                                                                    Disruption of two novel genes by a translocation co-segregating
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L. (bases l to 6940)
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TOSILBREI QMVKETI QAMTI-QUIQPAKENGEREAAASCMTAGVHEAQA*
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/protein_id "AAA12302.1"
/db.xret-edi:4414876"
/translation "AA0AEREELAANHMPGGGPQGAPAAAGGGGVSHRAGSRDYLPPA
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/codon_start_1
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A gene, disrupted in schizophrenia
Patent: wo 0140401-A 107-JUN-2001;
Akzo Nobel N.V. (NL): MEDICAL RESEARCH COUNCIL (GH): UNIVERSITY
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 7063)
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/db_xre1 "taxon:9606"
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/proddet "disrupted in Schizophrenia I protein"
/protein_id-"AAF73889.1"
/db_xret-"G1:8163869"
/translation="MPG99PQGAPAAAG993VSHPAGSFDYLPPAACFBRRKLARRPG
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/chromosome="1"
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Disruption of two novel genes by a translocation co-segregating
with schizophrenia
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1 (bases 1 to 7291)
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Taylor,M.S., Semple,C.A., Devon,R.S., Clair,D.M., Muir,W.J.,
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                                                                                                                                                                                                                                                         /product:"DISC1 protein"
/protein_id:"AAF7874 1"
/db_xref:"GI-8164836"
/translation "NUEWTAKDITEEIPSHTSEPERFERISKHIVESSPNVKKIGSV
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                                                                                                                                Direct Submission
Submitted (11 JAN 2000) Medical Genetics Section, The University of
Edinburgh, Crewe Road, Edinburgh EH4 2XU, Scotland
                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 33376)
Millar,J.K., Wilson-Annan,J.C., Anderson,S., Christie,S.,
Taylor,M.S., Semple,C.A., Devon,R.S., Clair,D.M., Mulin,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens DISC1 protein (DISC1) gene, partial eds
gene, partial sequence.
AF222987
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Millar,K., Anderson,S. and Christie,S
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 15002)
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Disruption of two novel genes by a translocation co-sequenating
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                                                                                                                                                                                                                                                                                                                       with schizophrenia
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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Porteous,D., Millar,K. and Hlackwood,D.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 4 from Patent W00140301.
AXI51213
                                                                                                                                                                                           A gene, disrupted in schizophrenia
Patent: Wo 0140301-A 4 07-JUN-2001;
Akzo Nobel N.V. (NL) ; MEDICAL RESEARCH COUNCIL (GB) ; UNIVERSITY
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Conservative
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/prodein_1d="AAP7.877.1"
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/transtation="LOERIKSLNISLKEITTKYCMSEKPCSTLRKKYNDIETQLPALL
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/gene="DISC1"
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on Oct 20, 2000 this sequence version replaced gi:10834423. During sequence assembly data is compared from overlapping clones Where differences are found these are unnotated as variations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_cleans/wormpop This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota: Metazoa; Chordata; Craniata; Verfebrata; Euteleostomi:
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPIIITH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/HGP/Chrl
RP4-584N17 is from the library RPC1-4 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was generated from part of bacterial clone contins of human chromosome 1, constructed by the sanger Centre Chromosome 1 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       annotated human repeat sequence elements (e.g. Alu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  feature key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 133968)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence is the entire insert of clone RP4-584N17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pCYPAC2
/note-"5 reads say 15 T's. 17 reads say 14 T's. Edited to 15."
                                                                                                          complement(90925...90983)
/note "Single clone region."
                                                                                                                                                                                                                          complement(90881. .90923)
                                                                                                                                                                                                                                                        assembly.
                                                                                                                                                                                                                                                                                                                                    /note-"Tandem repeat. Forced join. Assembly confirmed by restriction_digest." \ensuremath{\mbox{\sc T}}
                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RPC1-4"
17639
                                                                               /note "Single clone region. Sequenced from clone PCR only
Restriction digest confirms assembly."
                                                                                                                                                                  /noie="Single clone region. Sequenced from clone PCR only
Restriction digest confirms assembly."
                                                                                                                                                                                                                                                                   /note "Single clone region, Restriction digest confirms
assembly "
                                                                                                                                                                                                                                                                                                                29863.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone-"RP4-584N17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map-"q42.2-43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome-"l"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                             .29871
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BASE COUNT
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (24-FEB-1993) Linsenmayer T. F., Tufts University Medical School Anatomy and collusian Biology, 1% Harrison Ave. Bester. Massachusetts, USA, 02111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Type V collaren: molecular structure and fibrillar organization of the chicken alpha \mathbb{I}(V) NH2-terminal domain, a putative regulator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type V collagen, alpha 1 chain, NH2-terminal domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Linsenmayer, F.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Cell Biol. 121 (5), 1181-1189 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linsenmayer,T.F., Gibney,E., Igoe,F., Gordon,M K , Fitch, I M
Fessier,L.I. and Birk,D.E.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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be approximatly 200bp by restriction digest data."
40866 a 30073 c 26786 g 36243 t
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  471 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type-"connective"
/clone lib-"Lambda Zap"
/dev_stage="embryo"
                                                                           AQQQDDLDKDFTEETTKEYDGNYYYYYBPTVSPDTGPGMPANGGTTYEGTGGGAFAKEG
KGEPATTEPGMLVEGPPGPPGPAGLPGPPGPTGPVGLMGDPGFKGDPGAFKEGQ
                                                                                                                                                                                  QQLL. I VADPRAAHDYCEHYSPDCDTAVPDAPQSQDPNQUEYYTTIGEGEGUTYYY EY FY
                                                                                                                                                                                                           VKAKKGGOSFILISTYNEGGTOQTGVEMGRSPVET, PEPHTISK PIGPETET I DEFVEEGDT
                                                                                                                                                                                                                                                                                   /db_xref-"SPTREMBL:090589"
/translation-"MDTHTRWKRRSWIRNWQLHVALVIJGAAALGRAAEPADLEKVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone #105-1-1#
                                               PODPOTMEMEPERESOCODACSKOPMVSAQEAQAQATLQQAPEALRODACPMOLTOPE
                                                                                                                             PLVDEYNYETINEEYFTPLPYEDINYNEEVDPQGGLTENAVEAELPTSTVITYNETDA
                                                                                                                                                      YEDVDEAVKPEAPTTKPAPPGVAAGERPETKODYPXPTPSPEAGNPSPOTKGAAPVDD
                                                                                                                                                                                                                                                                FHNLPDG1TRTTGFCTSRRSSKEADVAYRVTKDAQLSAPTKQLYPASPFPFDFS1LTT
                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAA79882.1"
                                                                                                                                                                                                                                                                                                                                                                                                                         /product-"type V collagen, alpha 1 chain, NH2-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start+1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Standard name="type V collagen; alpha i chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Gallus gallus"
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                                                                                                                                                                                                                                                                                                                                              /db_xret -"G1:65434"
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  475 q
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PEATURES
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Matches 19; Conserv
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1 (bases 1 to 5575)
Gordon, M.K., Marchant, J.K., Foley, J.W., Idoe, F., Gibbey, E.P.,
Gordon, M.K., Marchant, J.K., Foley, J.W., Idoe, F., Gibbey, E.P.,
Nah, H.D., Barembaum, M., Myers, J.C., Rodriquez, E., Dublet, B., van
der Kest, M., Linsenmayer, I.F., Upholt, W.B. and Birk, D.E.
Complete primary structure of the chicken alphal (V) collagen chain
Matrix Biol 18 (5), 481-486 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-MAR-1999) Pharmacology and Toxicology, Rutgers College of Pharmacy, FORSI, Putgers University, 170 Frelinghuysen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gordon,M.K., Marchant,J.K., Foley,J.W., Iqoe,F., Gitney,E.P., Nah,H. D., Barembaum,M., Myers, J.C., Rodriquez,E., Dablet,B., van der Rest,M., Linsenmayer,T.F., Upholt,W.B. and Birk,D.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Road, Piscataway, NJ 08854-8020, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Enteleostomi;
Archosauria, Aves, Neognathae, Gallitornes, Fhasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chicken
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GPMGPPGSGGLKGEVGEMGPQGPRGTQGPPGPAGKPGRRAASDGARAGMPGQPGSLGRF
DRGFDGLAGLPGEKGNRGEPGPHGPPGPPGEPGERGNGFVGPRGTPGPPGGLTGRF
                                GPQGPAGGIGNPGAVGEKGEPGESGEPGLPGEVGLPGPKGERGEKGEAGPSGAAGPPG
                                                                                        PPGENGNKGETGEPGQKGSKGNKGEQGPPGPTGPQGPTGQPQPAGAINGEPGPRGQQGT
                                                                                                                                                   EGTKGTPGDAGI PGKINGPPGLPGEPGLPGLPGPIGSPGI KONEGPPGPPGPAGASENER
EGTKGTPGDAGI PGKINGPPGLPGEPGLPGLPGPIGSPGI KONEGPPGPPGPAGASENER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQGGDDLDKDFTEFTTKFYD&NYYYYDHTVSPDTGPXBANJOTTYFGJGGPXGEKGZ
KGEPATTEFDMLVEGPPGPEGPAGLPGPPGPTGPVGLMGDPGERGPFGRPGLEGADAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEDVDEAVKPEAPTTKPAPPGVAAGEKPETKQDYPXPTPSPEAGNPSKQTKGAAPVH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EHNLPPGTTKTTGF7TSKKSSKEAFVAYKVTKPAQLSAPTKQLYPASPEPEDFSTLTT
VKAKKGGQSELTSTYNEOGTOQTGVEMGKSPVFLYEDHTGKPGPEDYPLFKGTNLATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product "alpha l (V) collagen"
/protein_id "AAF28099.1"
/db_xref="Gi:6759903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism "Gallus gallus"
/strain-"breed White Leghorn"
/db_xret "taxon:9031"
PKGPPGDD3PKGSPGPVGFPGDPGPPGFPGPAGQINJPPGDKGDIXEFKGJTGSPGPIGF
                                                          <u> PGQKGDEGPHGFPGPPGPPGLGDGEKGETGDVGQMGPPGPPGPHGPSGPSAL</u>
                                                                                                                         ĠPAGSAĠP1GI ŁGKŁĘŁĠĘŁŁĠŁĄBAGEKĠAŁĠEKĠŁOĠPAGRDCI OGŁYGLŁGPAGŁYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .5508
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                                                                                                                                                                                                                                                                                                  All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996–1997)
http://ftp-genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilsen,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donneil,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, I., Karalas, A., Howland, J.C., Illev, I., Johnson, R., Johnes, C., Kann, L., Karalas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehorzky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGark, A., McKernan, K., McPheeters, R., Medirin, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., McCarthy, M., McCarthy, M., McCarthy, J., McCar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N. Anderson,S., Baldwin,J., Barna,N., Bastlen,V., Beda,F., Rouslavkiy,L., Boukhqalter,B., Brown,A., Rurket,G., Campopiano,A., Castle,A., Choepel,Y., Colangolo,M., Collins,S., Collymore,A., Cooke,P., DeArcllano,K., Dewart,K., Diaz,J.S., Dodge,S., Firlydh,W., Gage,P., Dodge,S., Gryette,M., Graham,L., Galaqan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC068340 166325 bp DNA linear HTG
Homo sapiens clone RP11 39516, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-MAY-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roy,A., Santos,R., Schaner,S., Severy,P., Spencer,B. Stange Thomann,N., Stojanovic,N., Subramanian,A., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on May 30, 2000 this sequence version replaced gi:7677711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                   Contact: sequence_submissions@genome wi mit edu
                                                                                                      Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                     Center code: WIBE
                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
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1 1562 c 1749 g 941 t 2 others
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SGLIPGPPGPPGEVI QPLP I QSSKTTRRN I DASQL VDJGNADNYMDYADGMEE I FG
SLINSLKLE I EQMKHPI LGTQHNPARTCKDI QI LGPPGPPGPKGAKGSSGPTGPKGE
EKGDRGLIPGPQGSAGPKGEQG I TGPSGP I GPPGPPGPKGAKGSSGPTGPKGE
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Project Information
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Pred. No. 1.3e+02;
0; Mismatches 2; Indels 0
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SCHROE

\* NOTE: This is a 'working draft' sequence. It currently \* consists of 29 contigs. The true order of the pieces \* is not known and their order in this sequence record is Chemistry: Dye-terminator Hid Dye: 100% of reads Assembly program: Phrap: version 0.960731 consensus quality: 148057 bases at least 040 consensus quality: 156781 bases at least 040 Quality coverage: 3.8 in Q20 bases: agarose-tp quality coverage: 3.9 in Q20 bases: sum-of-contins Consensus quality: Center clone name: 395\_1\_6 Insert size: 170000; agarose-fp Insert size: 163525; sum-of-contigs Sequencing vector: M13; M77815; 100% of reads 160697 bases at least Q20

\* arbitrary. Gaps between the contigs are represented as \* runs of N, but the exact sizes of the gaps are unknown. \* This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.

104495 104594; gap of 83244 934 93420 93519: 24754 74121 74220: gap of 100 bp 74221 83143: contig of 8923 bp in length 65674 65773; gap of 100 bp 65774 74120; contig of 8347 bp in length 83144 83243: gap of 56821 46347 46446: 41679 41778: 34056 372 37280 37379 34056 37279; contig of 3224 bp in length 24664 24763 gap of 21380 21479 · 21480 246 10868 10967: gap of 100 bp 10968 13422: contig of 2455 bp in length 13423 13522: gap of 100 bp 13523 15543: contig of 2021 bp in length 6994 8609: contig of 1616 bp in length 8610 8709; qap of 100 bp 8710 9718: contig of 1009 bp in length 9719 9818: qap of 100 bp 100 bp in length 9819 10867: contig of 1049 bp in length 37380 28765 28665 28764 15644 171 17161 17260: 2639 3729. .... 100 mp 3730 3829; gap of 100 mp 3830 5231; contiq of 1402 bp in length 17261 15544 15643. 6894 6993: 2539 2638: gap of 100 bp 2639 3729: contig of 1091 bp in length 1253 1352; gap of 104494: contiq of 10975 bp in length 116550: contig of 11956 bp in length 93419: contig of 10176 bp in 46346: contig of 4568 bp in length 179 gap of 100 bp 24663 contig of 3184 bp 200: gap of 100 bp 21374: contig of 4119 bp in length 543· gap of 100 bp 17150: contig of 1517 bp in length 65673; contig of 8853 bp in length .46: gap of 100 bp 51724: contig of 5278 bp in length 41678: contig of 4299 bp in length 64-gap of 100 bp 33955-contig of 5191 bp in length 28664: contig of 3901 bp in length 3: qap of 100 pp 8609: contig of 1616 bp in length 1: gap of 100 bp 6893: contig of 1562 bp in length 2538: contig of 1186 bp in length 1252: contig of 1252 bp in length qap of gap of dq 001 100 pp 100 bp 100 bp 100 bp 100 bp in length length

Center project

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15644. .17160
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5332, .6893
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17261. .21379
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/db_xref="taxon:9606"
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74221, .83143
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Best Local Similarity 90.5%;
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Sequencing vector: M13; 47%
Sequencing vector: plasmid: 53%
Chemistry: Dye-primer ET: 0% of roads
Chemistry: Dye-terminator Big Dye; 100% of roads
Assembly program: Phrap; version 0.990319
Consensus quality: 17305 bases at least Q40
Consensus quality: 177343 bases at least Q30
Consensus quality: 179974 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (15:SEF 2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Fark Parkway, St. Louis,
                                                                                                                                                                                                                                                  * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently 
* consists of 16 contigs. The true order of the pieces 
* is not known and their order in this sequence record is
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Homo sapinus chromosome 4 clone RP11-39516, WORKING DRAFT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site:http://genome.wnstl.edu/qsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of Homo sapiens clone
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Fred. No. 1.
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unknown
               of 1202
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                 length
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FEATURES
Db 112453 GGCTAAAGAGCTCACAGAGGA 112473
                                                                                                                                        ORIGIN
                                                                                                                                                       HASE COUNT
                                                              Matches
                                                                        Ouery Match 84.8%; Score 17.8; DB 2;
Hest Local Similarity 90.5%; Pred. No. 1.2e-02;
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/note-"assembly_name:Contiq29"
[85582. .186927
/note-"assembly_name:Contiq8"
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10346. .11861
                                                                                                                                                                                                                                                         20981. .184505
/motermassembly_name:Contig43
                                                                                                                                                                                                                                                                                                             /note "assembly_name:Contig41"
19214. .20880
                                                                                                                                                                                                                                                                                                                                          /note "assembly_name:Contiq40"
16714, .19113
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15256. .16613
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/chromosome:"4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism "Homo sapiens"
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                                                                                                                                                                                                                                vector_side:right"
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                                                                                                                                                                                                                                                                                                                                                                                                                    /note "assembly_name:Contig38"
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185481: contig of 876 bp in length
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contig of 1358
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contig of 1519 bp in length
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config of 1360 bp in length
                                                             0; Mismatches
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contig of 1667 bp in length
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                                                                                        DB 2; Length 186927;
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                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
                     Query Match 84.8%;
Best Local Similarity 90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
  Matches
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                                                                                                                                                                                                                                                                                                                                                  misc_teature
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  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (31-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBHO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 4, 2002 this sequence version replaced q1.18476874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL645615 197864 bp DNA linear HTG 01:FER: Mus musculus chromosome 11 clone RP23 395B22, *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 197564; sum-of-contigs
Insert size: 206991; 10.1% error; agarose-fp
Quality coverage, 16.49x in Q20 bases; sum-of-contigs Quality
coverage: 16.07x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye terminator Hig Dye: 100% of reads Consensus quality: 196787 bases at least Q40 consensus quality: 197011 bases at least Q40 consensus quality: 197213 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * be preserved
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* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Wellcome Trust Sanger Institute
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazōa; Chordata, Craniata; V∾rtobrata; Eutoleosfomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL645615.8 G1:18491384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (sites)
  Conservative
                                                                                                                                                                                                                                                                              /note="assembly_tragment:03474
tragment_chain:1"
154792. .164428
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fragment_chain:1"
164529...197864
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/chromosome="11"
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                     Score 17.8; DB 2; Length 197864; Pred. No. 1.2e+02;
  Mismatches
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    Indels
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                                                                       Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-APP-2000) to the EMRL/Conseque/CDDRI dat Haises
Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
Marine Biological Laboratory, 7 MBL Street, Woods Bole, MA 02543-1015, USA
                                                                                                                                                                                                                                                                                                                               * However, it should not be assumed that this clone * will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                        * contiqs. Runs of N are used to separate the reads * and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C.,
Hinkle G., Holder M.E., Sogin M.L.;
"Siardia: a model for ancient eukaryotic genome analysis",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG: HTGS_PHASEO.
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09-APP-2000 (Rel
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                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                * the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                           * overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                         * arbitrary. Low-pass sequence sampling is useful for * identitying clones that may be gene rich and allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This record contains 1 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McArthar A.G., Morrison H.G., Nixon J., Eakin N.Q., Kim U.,
Hinkle G., Holder M.E., Sogin M.L.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Capublished.
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/strain "WB-C6"
/clone-"AJZ051"
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Analysis of Notl flanking sequences: a new tool for good discovery
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## SUMMARIES

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### ALIGNMENTS

PASE COURT	FEATURES SOURCE		TITLE JOURNAL COMMENT	SOURCE ORGANISM REFERENCE	BF338605 LOTHS DEFINITION ACCESSION VERSION
/organism. Homo Sapiens" /ot_xief "Laxon,9606" /clone="IMAGE:4182165" /clone="IMAGE:4182165" /clone="IMAGE:4182165" /clone="IMAGE:4182165" /clone="IMAGE:4182165" /clone="IMAGE:4182165" /tissue_type="qlioblastona with EGFR amplification" /tissue_type="qlioblastona with EGFR amplification" /tab_host="OHIOB (T] phaye-resistant)" /note="Organ: brain: Vector: pCMV SPORP6: Site_1: Not!; /site_2: Sall: Cloned unidirectionally. Primer: Olige d]. /site_2: Sall: Cloned unidirectionally. Primer: Olige d]. /Average insert size 1.57 kb. Constructed by Life Technologies. Note: this is a Ncl_CGAP Library." /41 a 221 c 180 q 237 t	http://image.llnl.gov http://image.llnl.gov http://image.llnl.gov High quality sequence stop: 708. 	Email: cgapbs-remail.nih.gov Tissue Procurement: David N. Louis, M.D. cDNA Library Preparation Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I M.A.C.E. Consortium/LLNL at:	NIH-MGC http://mgc nci nih qov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact. Eubert Strausberg, Ph.D.	EST. human. Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	#P338605 602034283F2 NCT_CGAF_Br964 Homo surions cENA close IMACTC418216 57, mRNA sequence. BF338605 RF338605   GF-11285010

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eufeleostomi;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 962)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MST clone distribution information can
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGKI), Shiraki
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier, L., Lennon, G.
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Mammmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
L. (bases l to 570)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-*Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism "Homo sapiens"
/db xret "GDB:3758011"
/db xret "taxon:9606"
/elone-"IMAGE:472009"
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The WashU-Merck EST Project
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H9476]
Soares_placenta_8to9weeks_2NbHP8to9W Hoomo sapitens ciNA
clone IMAGE.256428 5' similar to contains Alu repetitive element.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314-286-1800
Fax: 314-286-1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Source:
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148 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMAGE Consortium, LLNL
                     (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo." \,
                                                                                              /clone_lib "Soares_placenta_8to9wcks_2NbHP8to9w"
/dev_stage="two placentae: one from 8 weeks and another from 9 weeks post conception"
/lab_host="bH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pf7T3b (Pharmacia) with a modified polylinker; site_1: Not 1; Site 2: Fco Rt; lst strand cDNA was primed with a Not 1: oliqo(d1) prime; [5]
                                                                         the Not I and Eco RI sites of a modified pT7T3 vector
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A1139969/c
            FEATURES
                                                                                                                                                                                          REFERENCE
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                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                             TITLE
                                                                                                                                                                         AUTHORS
source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 6.4%; Score 442.2; DB 10; Length 592;
Local Similarity 89.5%; Fred. No. 3.4e 72;
hes 527; Conservative C Missarvitus 50, Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 TCCCAAGAANNTGNGGTTAGAGGGATTTG-CACCGGGGGGGGGGGGGGTTTTTTGTATTTTTA 61
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                                  qa47a08.xl Soares_NhHMPi_Sl Homo sapiens กาฟล กไกกะ เฟลเซะได้หังหัวหั
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria, Primates, Catarrhini; Hominidae; Homo. 1 (bases 1 to 428)
                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                   TS3
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                         High quality sequence stop: 428.
                                                                                                                             Unpublished (1997)
                                                                                                                                                xebn1 eneB rommT
                                                                                                                                                      NCT-CGAP http://www.ncti.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                 AI139969.1 GI:3647426
                                                                                                                                                                                                                                                                                                           3', mRNA sequence
          Incation/Qualifiers
. 428
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Best Local Similarity 98.8%; Pred. No. 2.2e-68;
                                                                                                    ORGANISM
     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6790 tatglaattcaatacttttaacttttaatatcctcaccttatctaatctttqaatcttqaattttqtc 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6670 ctqqqxtgact11cttgaaqa1cxtcatccaattqqtqtttttcaqaaqtqttccaatqt 6729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         6910 aggcaaaa 6917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 TATGAATICIGIGIFIGIGGAGAAAAGCAACCATGCATTACIGGFCAAFGCCTTCTTGTA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   428 GAAAGETTOOTTAGOAAGI CAAAGAAAD EGAGEETTOOTAGOAAAAAAAAAAAGGCTTCCCACACTG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 OTGGGCTGACTTTCTTGAAGATCCTCATCCAATTGGTGTTTTTCAGAAGTGTTCCAATAT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 TATGTAATTCAATACTTTTACTTTTAATATCCTCACCTTATCTAATCTTTGAATTTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                         8 AGGCAAAA 1
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 446)
NCI-CGAP http://www.ncbi.nlm.nih.qov/ncicgap.
                                                                                                                                                                                                                                                   AW297205 446 bp mRNA libear EST 16-JAN-UT-H-FW0-ajd-f-01-0-HT-s1 NOT_OGAP_Sub6 Homo sapiens cDNA clone
                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertehrata; Euteleostomi;
                                                                                                    Homo sapiens
                                                                                                                              human
                                                                                                                                                         EST
                                                                                                                                                                                                      AW297205
                                                                                                                                                                                                                           IMAGE:2731513 3', mRNA sequence.
                                                                                                                                                                              AW29/205.1 CI:6/03841
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a 74 c 96 q 124 t 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro Following HAP purification, this DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_'ype "Pecked human melanseyte, tetal heart, pregnant uterus"
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/clone_lib-"Soares_NhHMPn_S1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ourry Match 6.0%; Score 418.4; DB 9; Length 446; Best Local Similarity 99.8%; Pred. No. 9.5e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soutce
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                                                                                                                         87 GAGGCCGGGCTACATGAGAAGCTCGACAGGGCCTGGGATCGGGTTCCTTTCCCCAGCAGT 146
                                                                                                                                                                                                                                                                                    27 COCAGGGAGCCGGGAFTGCTFACCACCTGCAGCGTGCFFTCCGGAGGCGGCGGCGGCTGGCACG 86
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail_cDNA_Library Preparation: M.B. Soares Lab Clone distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Stransberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCL CGAP clone distribution intormation can be tound through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence contained an oligo-dT track that was present in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cqapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hybridization with and river comprision: the IMAGE pool (NCI_CGAP_Kid3 pool | LLAM 334-3387, 389-368); 3798-3603 (IMAGE Clone(DS 142376-132391).

1456008-1456775, 500552-1502855); NCI_CGAP_Kid5 pool | LLAM 338-3442, 3722-3725, 3776-3778 (IMAGE Clone(DS 1323912-132584), 1471368-1472903, 1492104-1493255); NCI_CGAP_LU5 pool | LLAM 4575-3582, 3851-3854 (IMAGE Clone(DS 1444920-147791, 1520904-1522439); NCI_CGAP_LU5 pool | 1.1AM 4575-3582, 3851-3854 (IMAGE Clone(DS 1444920-147791, 1520904-1522439); NCI_CGAP_GC4 pool | 1.1AM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clone(DS 1068-2706-125864), 1469064-1479983, 1475592-147674-3); NCI_CGAP_FOOS-1258641, 1469064-1479983, 1475592-147674-3); NCI_CGAP_FOOS-1258641, 1469064-1479983, 1475592-147674-3); NCI_CGAP_FOOS-11, LLAM 2457-2459, 2758-2759, 3662-3668 (IMAGE Clone(DS 985608-886759), 1101192-1101959, 1217928-1-122615); NCI_CGAP_FOOS-10, LLAM 2647-26459, 2758-42-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-15-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-25-2712459, 27108-27108-27108-27108-27108-27108-27108-27108-27108-27108-27108-27108-27108-27108-27108-27108-27108-27108-27108-27108-27108-27108-2710
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Library had 7 million recombinants. A single-stranded DNA
preparation of BW was used as a tracer in a subtractive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZHOID-"Vector: PTŽTSD-Pac (Pharmacia) with a modified polylinker; Site_I: Not I; Site_E: ECO RI; NCI_CXAF_Sub6 is a subtracted library derived from HW, which consists of a mixture of four normalized libraries: NCI_CGAP_Brn50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host "DH10B (Life Technologies)"
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    Mismatches

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sapiens genomic clone Plate*2262 Gol 4 kow D, DNA sequence.
AQ442402
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Class: BAC ends
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HAC end Web Server: http://www.htsc.washington.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: 2262 row: D_column: 4
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(206) 616-3887
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                                                                              /moter forgan: sperm; Vector: pHeloRACTT; BAY Clones in E-COli DHIOH"
                                                                                                                                                                                                                                            /sex "male"
                                                                                                                                                                                                                                                                                                                                                        /clone_lib_"CIT Approved Human Genomic Sperm Library D"
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/clone "Plate 2262 Col·4 Row.b"
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                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1995)
Contact: Wilson PK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metaroa; Chordata; Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                          High quality sequence stop: 376.
                                                                                                                                                                                                                        This clone is available royalty free through LLNE, contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: ml3 -40 forward
                                                                                                                                                                                                                                                                      High quality sequence stops: 376 Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
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                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
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                                                                                                            /db_xref="GDB:3894931"
/db_xref="taxon:9606"
/clone="IMAGE:276555"
/lab_host="DH108 (ampicillin resistant)"
/hote="Vector, pT7T38 (Pharmacia) with a modified
polylinker V_TYPE, phagemid, Site_1, Not I, Site_
                                                                                                                                                                                          Location/Qualifiers
                                            /tissue_type-"multiple sclerosis lesions"
/dev_stage="Age 46"
                                                                               /sex-"male"
                                                                                              /clone_lib="Soares_multiple_sclerosis_2NbHMSP"
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                          Ph.D
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 366)
                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicqap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                 nx53~08 sl NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1265966.
                                                                                                                                                                                                                                                                                                                                                                                                                                            VV25646
                                                Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
                                                                        Email: cgapbs-r@mail.nih.gov
                                                                                           Contact: Robert Strausberg, Ph D
                                                                                                               Unpublished (1997)
                                                                                                                                         Tumor Gene Index
                                                                                                                                                                                                                                                                                                       human
                                                                                                                                                                                                                                                                                                                                                AA729949.1 GI:2751308
                                                                                                                                                                                                                                                                                                                                                                          AA729949
                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence
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cDNA Library Preparation: David B. Krizman, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              normalization to a Cot. = 5. Library constructed by Bento Scares and M.Fattina Bonaldo. SEA fine 4 calliple sclenosis lesions from one patient was kindly provided by Dr. Mewin C. Becker (NINES,NIH). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a Recker (NINDS/NIH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer [5'
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chNA Library Arrayed by: Greq Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution. NCT-CGAP clone distribution information can be

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PEATURES
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Best Local Similarity 99.2%; Pred. No. 4.4e 57;
                                                                                                                                                                ORGANISM
                                                                                  AUTHORS
  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 GACTTTCTTGAAGATCCTCATCCAATTGGTGTTTTTCAGAAGTGTTCCAATATTATGAAT 187
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                                                                                                                                                                                                                                                                                                                                                                                                                 6 AAATAA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 328 - Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the L.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                    yw58c07.sl Soares placenta_8to9weeks_2NbHP8to9W Home Sapiens cDNA
clone IMAGE:256428 47, mRNA sequence.
                                                                         Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                          H94731.1 G1:1102364
                                       .M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Ritkin,L., Robling,T., Soares,M., Tan,F., Trevaskis,E., Waterston
                                                                                             Mammalia; Entheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                   uruman
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
,R., Williamson,A., Wohldmann,P. and Wilson,R
The WashU-Merck EST Project.
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52 c 81 q 111 t
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/tissue_type "alveolar rhabdomyosarcoma"
/lab_host "DH108"
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DEFINITION AGENCOURT_6463821 NIH_MGC_71 Homo sapiens chan clone IMAGE:5517805
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                                                                                                                                                                                                                                                                                                                                                                    6547 etgecaggagagecteactgtgaagtetaggeteagaeaggeateaaeaaaeetatteae 6606
                                                                                                                                                                                                                 6847 gteatgtaatttattgetteattaaggttaet 6878
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                                                                                                                                                                                                                                                                   92 GTATATGTAALICAATACTTTTACTTNIAATATCCTCACCTTATCTAATCTTTGAATITL 😣
                                                                                                                                                                   32 GTCATGTAATTTATTGCTTCATTAAGGTTACT 1
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Seq primer: Promeda -21m13.
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Fax: 314 286 1810
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Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-tree through LLNL; confact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Source: IMAGE Consortium, LLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Pharmacia). Library constructed by Bento Sodies and M.Fatima Bonaldo."
a 79 c 106 q 114 t 9 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       double-stranded cDNA was size selected, ligated to Eco Ri
adapters (Pharmacia), digested with Not I and closed into
the Not I and Eco RI sites of a modified pTTT vector
the Not I and Eco RI sites of a modified pTTT vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev stade "two placentae: one from 8 weeks and another from 9 weeks post conception"
[lab_host "DHIOB (ampicillin resistant)"
/note "organ: placenta; Vector: pf7T4D (Pharmacia) with a modified polylinker; Site_1: Not 1: Site_2: Eco kl: 1st strand cDNA was primed with a Not 1 oliqu(dT) primer [5]
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KEYWORDS
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TITLE
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                                                                                                                                                                                                            4093 ragetgggaeteetattgagaragetgeaaaaraggetgattteaattaggeageaette 4152
                        4153 craaagtgractgaggaaggtggccccaagagaagctctctaaacaaaaggagtaccctct 4212
                                                                                                                                                                                                                                                                                                                                                                                                                3973 geragtaeteagtaetataagtaetgagtaettatataggeaatgtagtaeteagtaaat 4032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 CARCTRIGRACTCCTATTRIARIACARCTRICAAAACARRICTRIATTTCAATTARICAGCACTTC
                                                                                            303 CCATAGTGCACTGAGGAAGGTGGCCCCACTAAAACCTCTCTACAC-ACGGAGGACCCTCT 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGCTTAGTAACACAGTGTAGTGCTCAGTAGGAGAGCATAGTACTCAGTAACACAGGGCA 122
CCGGACCAGTACCTTTGGGAAATATACCCTACCATAA 398
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Plate: LLAM12177 row: j column: 14
High quality sequence stop: 170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cONA Library Preparation: Life Technologies, ite. cona Library Arrayed by: The L.M.A.G.E. Consortium (LINL) DNA Sequencing by: Agencourt Boscience Corporation Clone distribution: MWC clone distribution information can be found through the L.M.A.G F. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l (bases 1 to 1457)
NHH-MSC http://marchei.nib.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
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Tissue Procurement: AFCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref:"taxon:9606"
/clone="imAGE:5517805"
/clone=lbb "NH_MC271"
/clone_lbb "NH_MC271"
/rissup_lypa="lblomyosarcoma"
/lab_bast:"UllOB (phage resistant)"
/lab_bast:"UllOB (phage resistant)"
/note-"organ: uterus: Vector: pCMV-SPORT6: Site_1: Not1:
Site_2: sall: Cloned unidirectionally. Primer: Oligo dT
Average insert size 2.1 kb."
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RESULT 1 AA418180

밁 οy 밁 Ş 5 COMMENT PEFFRENCE SOURCE ORIGIN BASE COUNT FEATURES KEYWORDS VERSION DEFINITION AUTHORS ORGANISM TITLE Matches Query Match 6319 tttttctaagqcacaqagctqqtaaaatqtqaaqtaataqtqaacctaacaqtcaqaqac 6378 source 6259\_caaccttataaggaaggtgtttgtagatgafgcaacfgagcettaagaggaacfaattccc\_638 6499 yttäyyyäytvääayäaantyayentyyyyelaaanyayynttennanantyin äyyyyyy 65886379 aggeageatgetettaaetagtgetetteetaaagtteetttaatgteertittgagalii 6438 121 / Match 4.8%: Score 334; DB 9; Local Similarity 190.0%; Prod. No. 5.2e-52; 1 CAACCITATAAGGAAGGTGTTTGTAGATGATGCAACTGAGCCITTAAGAGGACTAATTCCC 6.0 AGGCAGCATGCTCTTAACTAGTGCTCTTCCTAAAGTTCCTTTAATGTCCTTTTGAGATTT TTTTTCTAAGGCACAGAGCTGGTAAAATGTGAAGTAATAGTGAACCTAACAGTCAGAGAC 120 334: Hillier, L., Allen, M., Rowles, L., Dubuque, T., Gelsel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU, Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK Fukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euthereostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 334) Homo sapiens 5', mRNA sequence. AA418180 This clone is available royalty-free thrench HARL constant the MAGE Consortium (into image. Juni.gov) for further information. Seq primer: 28e1 rev2 FT from American High quality sequence stop: 314. Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108 AA418180.1 GI:2079990 Email: est@watson.wustl.edu Tel: 314 286 1800 Fax: 314 286 1810 Conservative 95 a reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of LM.A.G.D. clones 300332-265223, 340488-345479, and 484488-489479. /note-"Organ: mixed (see below); Vector: p1714: Fac (Pharmacia) with a modified polylinker (Site\_1: Not 1: Site\_2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (mclane-yte 2NbHM, premnant utorus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization pregnant uterus" /db\_kret-"taxon.3606" /clone-"IMAGE:767471" /lab\_host-"DH10B" /tissue\_type-"Pooled human melanocyte, tetal beart, and /clone\_lib-"Soares\_NhHMPu\_Sl" /organism-"Homo sapiens" Location/Qualifiers 0; Mismatches 81 g 87 t 0; Indels Length 334: linear EST 16-57 1997 areast the

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KEYWORDS
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                200 ACAAGTGTTCCAATATTATGAATTCTCTGTGTGGAGAAAAGCAAACCATGCATTTACTGG 141
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Mammalia: Entheria: Primates: Catarrhini; Hominidae: Homo.
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Seq.primer: -4009 from Gibeo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Arrayed by: Greq Lemnon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Emmert Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: egapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inote "organ: lund; Vector: pTTTH)-Pac (Pharmacia) with a modified polylinker; relasmid DNA from the normalized library NCI_CGAP_L05 was prepared, and ss circles were made in vitro. Following HAP purilication, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCK amplified cDNAs from a pool of 5,000 clones made from the same library (clonelbs 1414920-14179) and 1520904-1522449). Subtraction by Bento soares and M. Failing Bonaldo.
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/lab.host "DH10B"
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/clone "IMAGE: @82288"
/clone lib "NCL_CGAP_Lig4"
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                  6723 ccaatattatqaattotqtqttqtqqqqaqaaaaqcaaccatqcatttactqqtcaatqcct 6782
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Best Local Similarity 100.
Matches (12) Conservative
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6663 cetqacectqqqetqactttettqaaqatceteatecaattqqtqttffftcaqaaqtqtt 6722
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A1075754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: eqapbs-remail.nih.gov
This clone is available royally-free through LLNL; contact the
IMAGE Consortium (intogimage.llnl.gov) for further information.
Insert Length: 1409—Std Error: 0.00
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High quality sequence stop: 454.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host-"DH10H"
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                                                                                                                                               4.5%; Score 312; DB 9; Length 470; 100.0%; Pred. No. 6.4e 48;
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Search completed: September 20, 2002, 06:59:17 Job time: 10727 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Watch	% Query Match Length DB	₽₽	ID	Description
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#### ALIGNMENTS

RESULT

SOURCE ORGANISM AQ078498 LOCHS FEATURES COMMENT REFERENCE VERSION DEFINITION KEYWORDS TITLE AUTHORS 30,110,05 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostami; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 292)
Adams, M.D., Bounsley, S.D., Thao, S., Bass, S., Linber, K., Colden, K., Berry, K., Granger, D., Sub, E., Wible, C., Shizuya, H., Simon, M. and end search page:
http://www.tigitorg.cd/.humgon/.humgon/.humd/.humgon/ Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr. Bookwillo, MD 20850, USA Onpublished (1998) Other\_GSSs: CIT-HSP-2361M16 TF AQ078498 CIT-HSP-2361M16.TR CIT-HSP Homo sapiens genomic clone 2461M16. DNA Homo sapiens alsnos are available from Research Genetics (integressen.com). BAC Email: mdadams tigr.org Map Building Use of a random human BAC End Sequence Database for Sequence Ready Venter, J.C human AQ078498.1 GI:3439682 AQ078498 sequence. 301 838 0200 301 838 0200 /organism "Home Supiens" /db\_xref="axon.9606" /elene="2361M16" /elene=11b "CIT-HSP" /sex="Male" Location/Qualifiers /cell\_type="Sperm" linear des 20 Aug-1998

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         library availability, please contact Pieter de Jona (pieter de Jona med buffalo edu). Clones may be purchased from BACPAC Resources (bitp://decpare.med buffalo edu/ordering) or from Research Genet es (info@resqen.com). BACC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
Contact: Shaying Zhao, William Micrman, Mark Adams
Department of Enkaryotic Genomics
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l (bases l to 620)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bhaili qenome-res@qsc.riken.qo.jp,
URL:http://qenome.qsc.riken.qo.jp/
Carninei.p., Nishiyama,Y., Westover,A., Itoh,M., Nadaoka,S., Sasaki
N., okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Contact: Yoshihide Hayashizaki
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modified pBluescript KS(+) after bulk excision from Lambda
                                            to Rot 20.0 and subtraction to Rot 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5] databatacamic Trickactinamina received at 1. cDNA was cleaved with XhoI and BamHI. Vector: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="10 days neonate"
/lab_host "DH10H"
                                                                                                                                                                                                                                                                                                              prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
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                                                                                                                                                                                                                                                             cap-trapper, cDNA went through one round of normalization
                                                                                                                                                                                                                                                                                                                                                                                                                       primed with a primer [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN. Division of Experimental Animal Research in Riken
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Fax: 216 361 9596
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a 130 c 83 q 68 t 8 others
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                                          Seq primer: TE
Seq primer: TE
Class: sheared ends.
Location/Qualifiers
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Unpublished (2001)
Other_GSSs: HOGZB41TK
                                                                                                                                                  Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                 Unpublished (2001)
Other_GSSs: BOHEE38TR
                                                                                                                                                                                                                                                                                               1 (bases 1 to 790)
Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
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DNA is from a doubled haploid provided by Tom Osborn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3523
Fay: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Chris Town
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Spermatophyta; Madnoliophyta: eudicotyledons: core eudicots;
Rosidae; eurosids II: Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                               Contact: Chris Town
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                                                                                                                                                                                         2 Medical Center Drive, Rockville,
                                                                                                                                    cdtown#tiqr.org
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/strain-"Tol000DH3"
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/Strain-"Tolo000H3"
/dk_xrc: "Luxen:2712"
/elone-"BedZB41"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           imail: genome resequenciae, riken.go.jp, mud.thtp://genome.gsc.riken.go.jp, carninei.p., Nushiyama, y., Westover, A., Itoh, M., Nagaoka, S., Sasaki v., N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y., Thermostabilization and thermostivation of thermolabile enzymes by trebalose and its application for the synthesis of full length conn. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(OSC), Yokobama Institute
The Institute of Physical and Chemical Research (RIKEN)
1.7-22 Suchiro-cho, Tsurumi ku, Yokobama, Kanadawa 230-0045, Japan
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Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN Monse ESTs (Konno, H., et al.)
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                                                                                                                                                                                                                                                                                   system, Genome Res. 9 (5), 463 470 (1999)
                                                                                                                                                                                                                                                                                                                                                                                        Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                        further details
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                                                                                                                                         Please visit our web site (http://demonse.rtc.rikeb.do.jp) for
                                                                                                                                                                                                         High etticiency full length cDNA cloning. Methods Enzymol. 303
                                                                                                                                                                                                                                                  Carminei, P. and Nayashizaki, Y
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/organism "Mus musculus"
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/clone "IMAGE:5254178"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                  source
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Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                  High quality sequence stop: 419.
                                                                                                                                                               http://imaqe.llnl.gov
Plate: LLAM11642 row: b column: 03
                                                                                                                                                                                                                    tound through the L.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                             Email: cqapbs-r-mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murimae; Mus
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                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc
                                                                                                                                                                                                                                                                                                 CDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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/clone_lib="KIKEN full-length enriched, adult male urinary
bladder"
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GAGAGAGAGAGAGCTCTTTTTTTTTTTTTTTTTTTYN 3], cDNA was
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
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/dev_stage "adult"
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/strain "CZECH 11"
/db_xref "taxon:10090"
                                                                                                         Location/Qualifiers
                                                        /ordanism "Mus musculus"
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Best Local Similarity 90.0%; Prod. No. 5.80*92; Length 400;
Matches 18; Conservativo 0: Migmatches 2: Indols 1
                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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233 GCTANAGACCTCCCAGAGGA 214
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                                                                         18: Conservative
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Ihmestrasse 73, Herlin, 14195 Germany
The CDNA libraries (CREP 522 and 524 were normalized with
Dictionacteotide Lingerprinting, resulting in a unique subset of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eickhoff,H., Schuchhardt,J., Ivanov,I., Meier-Ewert,S., O'Brien,J., Malik A., Tandon,N., Wolski,E., Pohits,E., Nyarsik,L., Reinhardt,R.
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Mammalia; Euthoria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/tissue_type="embryo"
/dev_stage="9 and 12 pe embryo"
a 114 c 112 g 98 t
                                                                                                                                                                                                                                                                    /strain "Black 6"
/db_xrot="taxon:10090"
/clone="R9222B55"
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Michigan State University
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B215 Anthony Hall, East Lansing, MI, USA
Tel: 517-355-8443
                                             Michigan State University
                                                                 Department of Animal Science
                                                                                          Unpublished (2002)
Contact: Jianbo Yao
                                                                                                                                       skeletal muscle cDNA library
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Tel: 517-355-8444
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/note="organ: bind limbs; Vector: pSPeKI1; Site_1: Not1;
Site_2: Sall"
a 127 c 109 g 111 t
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/dev_stage-"45 d and 90 d of gestation, birth, 7 wk and 1
yr of age"
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Hest total Similarity 90.0%; Pred, No. 6.20002;
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                                                                                                                                                                                                                                                                                                                                    availability, please contact Picter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chorisory/barpac/or crinq_information.btm). BAC end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: yaojemsu.edu
Seq primer: M13 reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other GSSs: CH230 9F19.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Raltus norvegious
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                                                                                                                                                                                                                                               Class: BAC ends
                                                                                                                                                                                                                                                                    Plate: 9 row: F column: 19
Seq primer: 37
                                                                                                                                                                                                                                                                                                                  page: http://www.rigr.org/tdb/bac_ends/rat/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                               Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: szhaostigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
The Institute to Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat BAC End Sequences from Library CHORI-230 EcoRI segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Jong,P. and Fraser,C.M.
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breqeordis,E., overton,L., Russell,D., Chen,D., Riggs,F., o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Znote "organ; hind limbs; Vector; psPoRT]; Site_L: NotL; Site_2: Sall"
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/sex "male and temale"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualitiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="skeletal muscles"
/dev_stage="45_d and 90_d of_gestation, birth, 7_wk_and_l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xret="taxon:9823"
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                                                                                            /db xref "taxon:10116"
/clone "CH230 9F19"
                                                                                                                                             /organism: "Rattus norvegicus"
/strain "BN/SSNHSd/MCW"
                                                                                                                                                                                                                Location/qualitiers
/note "Vector: pTARBAC2.1; Site_1: EcoR1; Site_2: EcoR1;
                                                                     /clone lib "CHORI-230 Sequent l"
                    /cell type "Brain"
                                              /sex "Female"
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556 GCTAAAGACCTCCCAGAGGA 547
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                     18; Conservative
                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Lothar Hennighausen Ph.D., Chu Xia Deng Ph.D. cDNA Library Preparation: Lite Technologies, Inc. cHNA Library Arrayed by: The L.M.A.G.E. Consortium (d.N.) DNA Sequencing by: Incyte Genomics, Inc. clone distribution: MCC clone distribution information can be found through the L.M.A.G.E. Consortium/LLNL at: http://image.linl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence start: 3 High quality sequence stop: 593.
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Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Murinae; Mus.
1 (bases 1 to 594)
NIH-M3C http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                           for transquaic model: Xu et al., Nature Genetics 22, (1999). Note: this is a NCI_CGAP Library."
189 c = 168 q = 126 t
                                                                                                                                                                                                                                                                                               samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference
                                                                                                                                                                                                                                                                                                                     Juste-"Organ: mammary; Vector: pcMV-SPORT6; Site_1: Not1: Site_2: Sall; Cloned unidirectionally primer: Olido dT. Average insert 2 kb. Library constructed by Lite Technologies; catalog #12017-018. Investigators providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type "tumor, gross tissue"
/lab_host-"DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib:"NIH_CGAP_Mam3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xret="taxon:10090"
/clone="IMAGE:5338175"
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                                                                                                                90.0%;
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565 GGCIAGAGAGCTCACCGAAG 584
                                                                                                                                                   Local Similarity
                       BE580834 Secopus laevis cocyte non normalized Xenopus laevis cocyte non normalized Xenopus laevis cONA clone IMAGD:3746182 57 Similar to TR:088383 088383 RGS12 PDZ-LESS
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
Web peaps at http://www.respen.org/Pipeass.teterpoor the id listed
below when ordering this clone. Source lab clone id xirnee003p23
Seq.primer: -40NP from Gibce
                                                                                                                        3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clitton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, M., Ritter, E., Jackson, Y., McCann, B., Waterston, R. and Wilson, R.
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BE680834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4444 Forest Park Parkway, Box 8501, St. Louis, MC 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Graniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Atrican clawed trog.
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                                                                                                                        Conservative
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a 142 c
                                                                                                                                                                                                                                                                                                                                                                      contruction by Bruce Blumberg (Blumberg et al., 1991
Science 253, 194-196; Hawlet et al., 1995, Genes Dev. 9,
2923-2935). Note: This is a Xenopus Gene Collection (XSC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chart "V. 19 of IRC setting St. Nite 1. 1904 NA. 27 Short chark was prepared from 1994 of poly A. RA. 28 Ecoki-Xhol out char was then ligated into Unizap-XP (Stratagene) with EcoRI at the 5' end and Xhol at the 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  excess driver by streptavidin sepharose chromatography, the ss-phagemids were made double stranded and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to biotinylated driver (prepared from the same librar-
PCR) to Cot-omega of 11. After removal of hybrids and
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Atissue_type "compto (studes 5 and 6)"
Alab_host="Top-10 r"
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/clone "IMAGE:3746182"
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                                                                                 Query Match 80.0%; Score 16.8; DB 9; Length 577; Best Local Similarity 90.0%; Pred. No. 6.6e+02; Matches 18; Conservative 0; Mismatches 2; Indels
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Washington University School of MedicineP
4444 Forest Park Parkway, How H601, St. La
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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenborg,K., Steptoe,M., Tan,F., Underwood,K., Moore,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniuta; Vertebrata; Enteleostomi; Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridue; Murinae; Mus. l. (bases 1 to 677)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Theising, B., Wylie, L., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE Consortium (into image. Hnl. gov) for further information.
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/clone:"IMAGE:577618"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type "Thynnus"
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Title:
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                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cun2 6/ptodata/2/ina/5A_COMR seq:*

2: /cun2_6/ptodata/2/ina/5B_COMB.seq:*

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5: /cun2_6/ptodata/2/ina/PCTUS_COMB.seq:*

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Copyright (c) 1993 2000 Compagen Ltd.
SUMMARIES
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#### ALIGNMENTS

RESULT 1 US-08-960-756-1/c

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WOLFOLD : Aborroll
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542 5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHERENT APPLICATION DATA:
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SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/068003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/6 FILING DATE: 04-JAN-1991 APPLICATION NUMBER: 07/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/2
FILING DATE: 21 MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/476,062A FILING DATE: 07 JUN-1995
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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; LENGTH: 5849
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NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Xu, Shuang yong
                                         TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
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PRIOR APPLICATION DATA:
ON TOWN NUMBER: US 08/583,808
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TITLE OF INVENTION: Methods and Reagents for Regulating
TITLE OF INVENTION: Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Andrews, William H. APPLICANT: Adams, Robert R.
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                    SEQUENCE CHARACTERISTICS:
                                                                                                       REFERENCE/DOCKET NUMBER: 015389-0012200S
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                            FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
                                                                                                                                                                                                                                                                                          FILING DATE: 05-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentln Release #1.0, Version #1.30
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: OTHER INFORMATION: /product= "TPC3"
US-08-710 249 3
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION FOR SEQ ID NO: 3:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0, Version #1.30
CUBRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 6
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/583,808 FILING DATE: 05-JAN-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                       FEATURE:
                                                                       MOLECULE TYPE: cDNA
                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/710,249 FILING DATE: 13-SEP-1996
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LOCATION: 79..1380
OTHER INFORMATION: /product = "TPC3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  California
                                                                                                                                       4080 base pairs
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US-09-220-157A-3
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                                                                                                                                                                                                                                                                                                               ; GENERAL INFORMATION:
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SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                   Sequence 33, Application US/09712266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 69.5%, Score 14.6, DB 4, Length 414; Hest food Similarity 81.5%, Prod No. 1.2002; Matches 17; Conservative 0, Mismatches 4, Indels
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                                                                                                                                                                                                                                                                                                                             Patent No. 6333158
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TITLE OF INVENTION: DNA POLYMERASE-RELATED FACTORS FILL REPERENCE: 1422-4089CT
CURPENT ADPLICATION NUMBER: US/09/712,266
CURRENT FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 09/446,504
PRIOR FILING DATE: 1999-12-23
FRIOR APPLICATION NUMBER: FOIL TH'M, 02845
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
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APPLICANT: KATO, Ikunoshi
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    Application US/09446504
6218150

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SATO, Yoshimi
FULITA, Tomoko
MIYAKE, Kazue
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KATO, Ikunoshin
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MIYAKE, Kazue
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; ORGANISM: Pyrococcus turiosus IIS 09 446 504 32
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TYPE: DNA
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LENGTH: 414
                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                Sequence 32, Application US/09712266
Patent No. 6333158
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Patent No. 6218150
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                 APPLICANT:
APPLICANT:
                                                                                       APPLICANT: UEMORI, Takash
APPLICANT: SATO, Yoshimi
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APPILICANT: SATO, Yoshimi
APPILICANT: FULUTA, Tomesko
APPILICANT: MIYAKE, KAZDO
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FRICK APPLICATION NUMBER: JF 9-320692
PRIOR FILING DATE: 1997-11-27
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FILLE OF INVENTION: DNA POLYMERASE RELATED FACTORS
FILLE REFERENCE: 1422-408PCT
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APPLICANT:
                                                                          APPLICANT:
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PRIOR FILING DATE: 1997-06-26
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ASADA, Kiyozo
                                                   FUJITA, Tomoko
MIYAKE, Kazne
 KATO, Ikunoshin
               MUKAI, Hiroyuki
ASADA, Kiyozo
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; Sequence 45; Application US/09318448
; Patent No. 6210950
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                                                                                                                                                                                                                                                                               US-09-318-448-45/c
                                                                                                                                                                                                                                                                                                    RESULT
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                  CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
                                                                                              APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
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APPLICANT: Stenioos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
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PRIOR APPLICATION NUMBER: JP 9-320692
PRIOR FILING DATE: 1997-11-27
                                                                    FILE REFERENCE: 601-1-057
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PRIOR FILING DATE: 1999-12-23
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NUMBER OF SECTIONOS: 46
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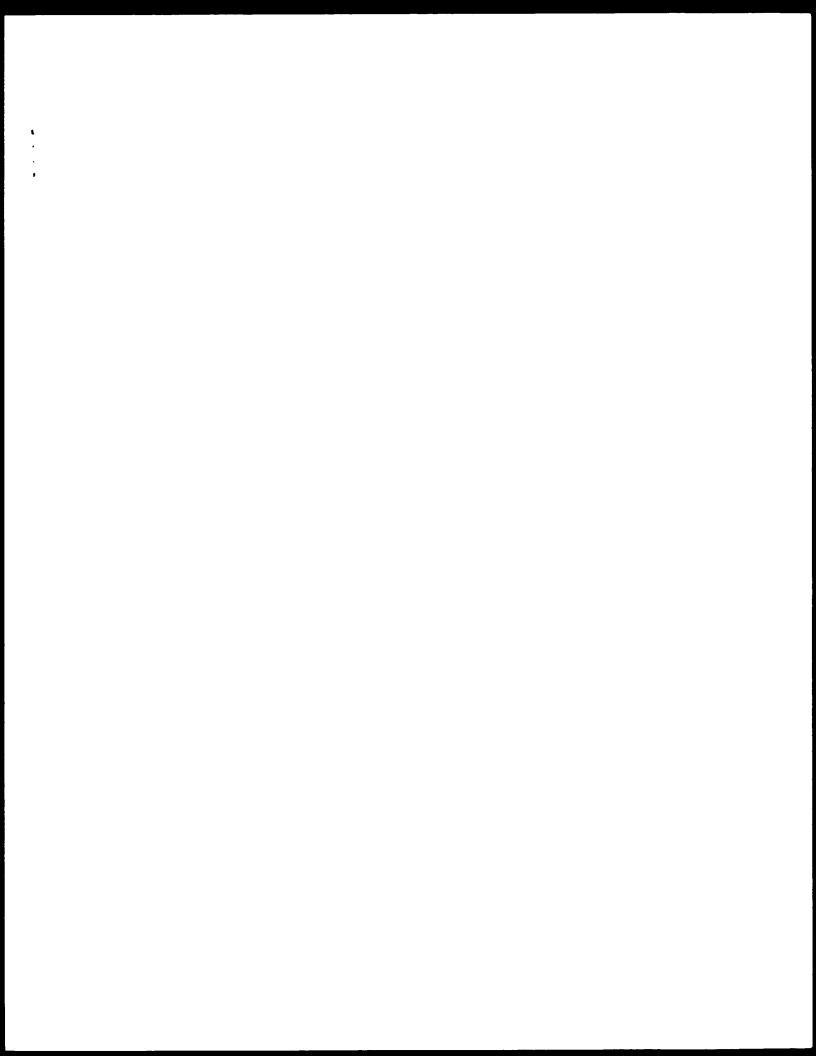
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: Fatest No. 6210950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEMERAL INFORMATION:
APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
APPLICANT: Stenroos, Edward S.
ITTLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 45
LENGTH: 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08313181 Patent No. 5681735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              whery Match 69.5%; Score 14.6; DB 4; Length 1275; Hest Local Similarity 81.0%; Pred. No. 1.3e+02; Matches 17; Conservative 0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEC ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guery Match 69.5%; Score 14.6; DB 4; Length 1273; Hest Local Similarity 81.0%; Pred. No. 1.3e+02; Matches 17; Conservative 0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENERAL INFORMATION:
APPLICANT: Goldhamer, David J.
APPLICANT: Goldhamer, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LITLE OF INVENTION: DEVELOPMENTAL DISORDERS FILE REFERENCE: 601-1-057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHFTWAKE: Patentin Ver. 2.0
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                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Transcription Control Element for INTLE OF INVENTION: Increasing Gene Expression in Myoblasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               703 GGGCAAAGACCTCACCGGGCA 683
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                                                                                                                                                                                                                                                                                               SIREET: 1601 Market
CITY: Philadelphia
                  APPLICATION NUMBER: US/08/313,181 FILING DATE: 07-00T-1994
                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                    CHUNTRY:
                                                                                                  SOFTWARE:
                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                               STATE:
CLASSIFICATION:
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                                                                                          Patentin Release #1.0, Version #1.30
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US-08-328-322-20
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US-08-313-181-2
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; Patent No. 5723436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 69.5%; Score 14.6; DB 1; Length 1757; Best Local Similarity 81.0%; Pred. No. 1.4e+02; Matches 17; Conservative 0; Mismatches 4; Indels 0
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                                                                                                                                                                                 TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: 2
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                 REGISTRATION NUMBER: P38,61
REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION RUMBER: US,
FILING DATE: 24-OCT-199
CLASSIFICATION: 530
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Huang, Laigiang APPLICANT: Cyert, Martha S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (215) 563-4100
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                                                   MOLECULE TYPE: DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Calcineurin Interacting Protein Compositions TITLE OF INVENTION: and Methods
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                   ORIGINAL SOURCE:
                                    HYPOTHETICAL: P
                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-1998/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: double TOPOLOGY: not relevant
                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
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INDIVIDUAL ISOLATE:
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                                                                                                          nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                          DNA
                                                                                                                                                                                                                                                                                                                                               24-OCT-1994
 DNA fragment containing
                                                                                                                                                                                                                                                                           P38,615
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US 07 864 475A 4
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MEDIUM TYPE: 8.5" DISKETTO, 1.44 Mb
MEDIUM TYPE: 8.5" DISKETTO, 1.55SX
OPERATING SYSTEM: MS DOS (VETSION 5.0)
SOPTMARE: WOLGHOLTECT (VETSION 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/02/854.475A
FILLIN: DATE: 04.06.1992
                                                                          Matches 17; Conservative
                                                                                             Overy Match 69.5%; Score 14.6; DE 1; Length 2010; Bost Local Similarity 81.0%; Pred. No. 1.40002;
                                                                                                              Outry Match
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APPLICANT: Jupper, Barald
APPLICANT: Forts, John T. [Jr.]
APPLICANT: Schipani, Ernestina
Title of INVENTION: PARATHYROID BERNONE RECEIPTOR
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                                                                                                                                                                                                                                                                                                                                  TELECOMMONICATION INFORMATION: TELEPHONE: (617) 542 5070 TELEPAX: (617) 542 8906
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/681,702
PILING DATE: 05-04-1991
AUTORREY/ADENT INFORMATION:
NAME: Fabl I. Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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783 GGCTGAGGGCCTCACCGAGGA 803
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                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fanl T. Clark
RESISTRATION NUMBER: 40,162
REFERENCE/DECKET NUMBER: 00786/071002
                                                                                                                                                                                                                   TYPE: macleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                         TENETH:
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                02110-2804
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Abou Samra, Abdul Badi
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Search completed: September 20, 2002, 10:34:45 Job time: 22219 see



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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Maximum Match 100%
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36 447 Million cell updates/sec
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Copyright (c) 1993 - 2090 Compagen Ltd.
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Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Watch	Whery Match Length DB ID	DB 	1D
۲ -	22.23	190.0 100 0	255 255 255 255	to to	AAK53267 AAK52293
٠.	22:	100 0	34780	10 t	AAH24652
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NBA16828 AARA2033 AARA2033 AARA2133 ABL24793 ABL24792	AAK79426 AAS92272 ABA16829 ABA16827 ABA16827	AA594879 AA104668 AAA34886 AAF21008 AAS40703 AA106606	AAC37729 AAC37729 AAC501479 AAC55427 AAC31599 AAC96066 AAC41506 AAAF21006 AAAF21006 AAAF21006	AAP61281 AAS59515 AAC98226 AAH03240 AAH03240 AAH03240 AAAH051848 AAH051848	AA159357 AAS73780 AAA53022
Human nervous syst Human incress/haema Heras Janusche haema Human ORFX ORF338 Drosophila melanoq Procophila melanoq	Homas Emerged to the Homas moved Homas moved that reveal syst Homas Emerged Homas Emerged Homas Environs Syst	Haman DNA Sequence Thermas plasmid pl Human adenosine re Human low adenosin DNA encoding human Bullan regroductive	Arabidopsis thalia Arabidopsis thalia Human secreted pro Nucleotide sequenc Flax SAD2 uene. I pl50.95 alpha saba Human low adonosin Human low adenosine Human necessine re	N. magadail bacter in Propionibacter in Propionibacter in Human colons cannet Human clank clone ( Thermas op. Tsp451 Homan clank sequence Artibleton thak sequence	Human polynucheoti DNA enceding novel Human beta-1,4-gal

#### ALLICNMENTS

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	09-AUG-2001, 05-FEB-2001; 03-FEB-2000, 27-AFP-2000;	Human: cytokine vascine, pedio vascine, pedio tissue growth i nervous system Homo sapiens.	AAK53267; Q5-NQV-2001 Human polysu	7 7 7
2000US-0598075. 2000US-0598075. 2000US-054936. 2000US-054936. 2000US-064936.	09-AUG-2001. 05-FEB-2001; 2001WO-US04098. 03 FEB-2000, 2000US-0496914. 27 AFP-2000, 2000US-0450975.	Human: cytakine, cell proliferation, vell differentiation; gene therapy, stancell growth factor; bromatopolesis; vascine, peptide therapy, stancell growth factor, immunomedulatory; cancer; leskaemia; nervous system disorder; arthritis; inflammation; ss. Homo sapiens.	AAKS4057; Q5-NOV-2001 (first entry) Humma polysuclectide SE2 ID M3 2796.	nada nada na

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AAK52283
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Ober Match
100.0%; Score 2): DB 2
Hest Lacal Similarity 100.0%; Pred. No. 0.78;
Matches 21: Conservative 0; Mismatches
                               0.4 FEH 2000;
27 APR 2000;
20 JUN 2000;
19 JUL 2000;
01 SEP 2000;
15 SEP 2000;
20 OTT 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                production of other cytokines in other cell populations. The polynucleofides and polypoplides are useful in gene therapy, vaccines or peptide therapy. The polypoptides have various cytokine like activities, e.g. stem cell drowth factor activity, bacmatopolesis regulating
                                                                                                                                                                                                                                                                                                                 vaccine; peptide therapy, stem cell-growth factor, hacmatopolesis, tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                                                                                                                                                                                                                                               AV 0617.510070M
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                                                                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliteration; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                      Human polymucleotide SEQ ID No 828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAKS228+ standard; cDNA; 2565 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         were missing at the time of publication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 4994 4995; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful in diagnosis and gene therapy
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                2000;
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Wand D, Wand J, Zhand J, Ren E, Chen R, Wand ZW,
Yand Y, We}hrman T, Goodrich R;
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RESULT
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Best Local Similarity 100.0%; Pred. No. 0.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production of other cytokines in other cell populations. The polynucleotides and polyneptides are useful in gene therapy, vaccines or peptide therapy. The polyneptides have various cytokine like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and may be useful in the diagnosis analog activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1809 ggctaaagaceteacegagga 1829
                                                                                                                                                                                                                                                                                                                                                     Disrupted in schizophrenia ! gene; DISI gene; schizophrenia
              (UYED-) UNIV EDINBURGH.
                              (ALKU ) AKZO NOBEL NV.
(MEDI-) MEDICAL RES COUNCIL
                                                                                  01-DEC:1999;
                                                                                                                                                  07 - JUN - 2001
                                                                                                                                                                                    WO200140301-A2.
                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                     psychiatric disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of a disrupted in schizophrenia 1 (DISI) gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH24651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH24651 standard; cDNA; 7063 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             were missing at the time of publication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to polymmelectides (AAK51456-AAK5445) and the encoded polympetides (AAM78328-AAM80402) that exhibit activity elating to
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                                                                                                                28-NOV-2000; 2000Wo-EP11915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C, Drmanae RT, Asundi V, Zhon P, Xu C, Cao Y
Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW:
Yang Y, Wejhrman T, Goodrich R:
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                                                                                                                                                                                                                  /product
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chromosome 1 inverted in a balanced t(1.11) (q42.1.q14.3)
translocation, and its encoded proteins, useful as medicament for
                                                 Disclosure: Page 39-50:
                                                                                                                                                           translocation, and its encoded proteins, useful as medicament for treating psychiatric disorders -
                                                                                                                                                                                                                                                                                 Novel isolated polynucle of the which currenteds a breakpoint chromosome I involved in a balanced t(1:11) (q42.1:q14.3)
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MEDICAL RES COUNCIL.
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39-JUN-2000;
07-JUL-2000;
07-JUL-2000;
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                                                                                                      14 - AUG - 2000;
14 - AUG - 2000;
14 - AUG - 2000;
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19-MAY-
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                                     14 - AUG - 2000;
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Matches 20; Conser
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number of human reproductive system related antiques. These can be used
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                   19-JUL-2001.
                                                                                                                                                       mat_peptide
                                                                                                                                                                                                     siq_peptide
                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                          Cushing's syndrome: developmental disorder: stroke; gene therapy; renal tubular acidesis; transgenic animal; cancer ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                     conqestive heart failure; angina pectoris; neurological disorder;
Huntington's disease; Alzheimer's disease; Parkinsen's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anaemia; intection; cardiovascular disorder; myocardial intarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ 1D No 39239; 3071pp · Sequence Listing; English
                                                                 WO200151646-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; SECP; cell proliterative disorder;
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294 GOGTANACACCTCACCCAGG 275
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554..907
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                                                                                                            /product- "Mature human SECP protein"
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                                                                                                                                                                                                                             "Buman SECP protein"
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     multiple sclerosis, myasthenia gravis, pancreatitis, uveitis, Werner syndrome and infections; cardiovascula; disorders such as congestive heart failure, myocardial infanction, ischaemic heart disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell proliterative disorders such as number, atteniosolenosis autoimmune/ atherosolenosis, cirrhosis, hepatilis, and psoriasis; autoimmune/ inflammatory disorders such as acquired immune deficiency syndrome (AIDS), altergies, automia, asthma, autoimmune thyroiditis, cichn's disease, diabetes mellitus, Goodpasture's syndrome, Grave's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-TAN-2000: 20000S-017773
29-JAN-2000: 20000S-0178832
02-FEB-2000: 20000S-0179774
03-MAP-2000: 20000S-0186792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acidosis and Cushing's syndrome. SECP DNA is useful to create knock-in humanised animals (pigs) of transperie animals (nice or rats) to model human disease. For the apertie of diagnostic purposes, for sematic or germline therapy, to generate hybridisation probes useful in mapping the naturally occurring genemic sequence, and in molecular biological techniques. The present sequence is human SECP cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           andina pertoris, neurological disorders such as stroke, Huntington's disease, Alzhelmer's disease, Pick's disease, epilepsy, dementia, and Parkinson's disease, and developmental disorders such as renal tubulat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and molecules enoughing such protoins. SECP agenist and/or antagenis is useful for treating diseases associated with decreased expression or overexpression of functional SECP. The disorders treated include
                              Human mostropic; immunosupprossant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Allaboumer's; Parkinson's disease; Humlinghtou's disease; Maemiostatle; amyotrophic lateral scierosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated human secreted protein useful for diagnosing, preventing and treating cell proliferative, autolemnune/inflammatory,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 112; 117pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JAN-2001; 2001WO-US00895
                                                                                                                                       Human polynucleotide SEQ ID NO 5132.
                                                                                                                                                                              22 KAT 2001
                                                                                                                                                                                                                         AA161143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1156 BP; 191 A; 388 C; 352 C; 225 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiovascular, neurological and developmental disorders
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Tang YT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                              (first entry)
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               thrombolytic, drug screening, arthritis
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Baughe MP In DAM Yai
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Best Local Similarity
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225 - APR - 2000; 20090US - 0552317
09- JUL - 2000; 20090US - 05628404
20090US - 0620312
03 - AUG - 2000; 20090US - 0653450
                                                                                                                                                                                                                                                                                                                                                                                                                           utilisation of the activities such as Immune System suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and assays for receptor activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Farkinson's disease, Huntington's disease, amyotrophic lateral systems and Shyterapa Syndrome. They uses include the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, used such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 5132; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 SER 2000; 2000US-0662191
19-00T-2000; 2000US-0693036
29 NOV 2000; 2000US-0727344
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                                          Human polynucleotide SEQ ID NO 1560
                                                                                                                                     AA159357 standard, cDNA, 1169 BF
                                                                                                                                                                                                                                                                                                                                                       Sequence 1167 BF, 186 A,
                                                                                                                                                                                                                                                                                                                                                                                    specification.
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P-PSDB: AAM41987.
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                                                                         22:0CT:2991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                 565 GGGIAAAGACCTCACCCAGG 546
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ote: The sequence data for this patent did not form part of the printed
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           mostropic,
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Zhou P,
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         inconesappressant
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Wedunan T,
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, Xu C, Xue AJ,
E, Drmanac RT;
                                                                                                                                                                                                                                                                                             Pred. No. 84;
                                                                                                                                                                                                                                                                                                           Score 16.8,
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        cytostation
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Yahq Y,
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         gene therapy; cancer;
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Chang J:
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peripheral nervous system;

neuropathy;

central nervous system; CNS;

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RESULT 11
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110 AAS232
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Best Local s
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          13 FEB 2002 (tirst entry)
                                                                                                                                                                                                                                                                            Sequence 1169 BP; 189 A; 391 C; 356 G;
                                                                                                                                                                                                                                                                                                          specification
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                                         AAS7 (780;
                                                                       AAS73780 standard; cDNA; 1171 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                            y Match 80.0%; Score 16.8;
Local Similarity 90.0%; Pred. No. 84;
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• JUL 2000;
• JUL 2000;
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                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed
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200008 -0653450.
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Zhang J;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (11). (11) is useful for generating and bodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a lood supplement. (11) and its binding partners are useful in medical imaging of sites expressing (11). (1) and (11) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polypurched ide sequences have applications in diagnostics, foreasies, gone mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and are no acid sequences. Asset 17-Asset 54 represent cover human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, torensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            numan; chromosome mapping; gene mapping; gene therapy; forensic; tood supplement; medical imaging; diagnostic; genetic disorder; ss
03-JAN-2001 (first entry)
                                                                              AAA53022 standard; cDNA; 1532 BP
                                                                                                                                                                                                                                                                                                                                                         Sequence 1171 BP; 192 A; 394 C; 357 G; 228 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotides are also used in diagnostics as expressed sequence tags tor identifying expressed genes. (1) is useful in gene therapy techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 9584; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-ocr-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding novel human diagnostic protein #9884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 MAR 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 MAR - 2001; 2001W0 - US08631
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                                                                                                                                                                                                                                                            18; Conservative
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                                                                                                                                                                                                                                                                           80.0%;
                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                               Pred. No. 84;
                                                                                                                                                                                                                                                                                                  Score 16.8;
                                                                                                                                                                                                                                                                                                    DH 24;
                                                                                                                                                                                                                                                            2:
                                                                                                                                                                                                                                                                                                  Length 1171;
                                                                                                                                                                                                                                                              Indels
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Human beta-1,3-galactosyltransferase znssp2 coding sequence

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DX DX AX E
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                                                                                                      AAF61
                                                                                                                     RES. 11
                                                                                                                                                                                                                                                                                                                                   ulcerative colitis, and disorders associated with cell migration, contact inhibition, tissue interactions, meuronal specificity, restilisation, embryonic cell adhesion, limb bud morphogenesis, mesenchyme development immede researching and provide and glycolipid biosynthesis. One possible method of ulreatment is the use of gene therapy. The degenerate version of this secures is also also also therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                         is a beta-1.3-galactosyltransforase, and is a type II membiane protein involved in cell-cell interactions. The yene is found on human chromosome 1943-2. The yene and protein can be used in the treatment of cancer, particularly motastases, inflammation, autolemonae diseases such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sid_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human: buta-1,3-qalactosyltronaferase, inssp2, cull cell intecancer; autoimmune disease, digestive disorder, gene thorapy; inflammation; chromosome 19q13.2; ss.
N. mayadaii bacteriophage phi-CH1 genomic DNA fragment #1
                                                                                                                                                                                                                                                                                              Sequence 1532 BP; 241 A, 545 C, 458 C, 287 T, 1 other,
                                                                                                                                                                                                                                                                                                                          sequence is also given (AAA53023).
                                                                                                                                                                                                                                                                                                                                                                                                                             as diabetes, digestive disorders including Crohn's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 94-97; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nove!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conklin DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYMO ) SYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-DEC-1999:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                             25-MAY-2001
                                                                                      AAF61281 standard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the coding sequence for human Znssp2. This
                                                                                                                                                               935 GGGTAAAGACCTCACCCAGG 916
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                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                         l ggctaaagacctcaccgagg 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2mssp2 polypoptides belonging to galactosyltransferase family for treating disorders associated with glycoprotein synthesis
                                                                                                                                                                                                                        Conservative
                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0208970
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154..1294
/*tag-__c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-
101..1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product = "Znssp2"
/transl_except= (pos.509..511,aa.Xaa)
/note=_"Xaa=unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                        80.0%; Score 16.8;
90.0%; Pred. No. 86;
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                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                   Length 1532;
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                     Gaps
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This invention describes a novel isolated nucleic acid (1) from the CC genome of phage phi CH1 of Natrialba magnadi. The groume of phi-CH1 is a CC combination of 48700 and 101948 base pair sequences (S1 and S2), both CC fully defined in the specification. The invention also describes a novel (1) recombinant vector (RV1) containing the ori of phi CH1; (3) cell CC (2) recombinant vector (RV2) (RV1) containing the ori of phi CH1; (3) cell CC (1); N. magadii cells free from the prophage of phi-CH1; (5) phage CC (1); N. magadii cells free from the prophage of phi-CH1; (5) phage CC variants having genomic sequences at least 70 % homologous with the CC phi-CH1 and having genomic sequences at least 70 % homologous with the CC phi-CH1 genome: (6) use of phi-CH1 as gene transfer vector; and (7) use CC vectors that contain (1) are used to transform halphilic Archaea. CC specifically N. magadii, for production of proteins and other polymers. CC cya. pulyflydraxibatylaty. Nectors containing (1) allow controlled, CC induction of proteins and other polymers.
Sequence 48300 BF, 10376 A, 14421 C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1c; Page 16 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid from phage phiChl, used to create vectors expressing proteins and polymers in halophilic \mbox{\bf Archaea} \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Witte A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LUBI/) LUBITZ W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 FEB: 2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natrialba magadii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage phi-CHl.
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                                                                                inducible expression of compounds in Archaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-AUC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99DE-1037719.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72pp; German.
15356 G;
8147
T; 0 other;
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Matriting
                                                      Best Local Similarity
                                                               Query Match
 5618
          2 getiaagaeeteaeegagga 21
gctgatgaceteaeegagga 5637
                                           Conservative
                                                      80.0%;
90.0%;
                                             ?
                                          Score iv., Pred. No. 1.1e+02;
                                                               Score 16.8;
                                                                 DB 22;
                                                               Length 48300;
                                           Indole
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AAS59515
                                                                                                  uveitis) endophthalmitis, bone, joint, central mervous system, hijsA;
inflammatory lesion; wene sulgaris; enzyme linked immunosorbent assay;
                                                                                                                                 SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; esteomyelitis
                                                                                                                                                                    Propionibacterium acnes immunogenic protein encoding DNA #10.
                                                                                                                                                                                                                                           AAS59515;
                                                                                                                                                                                                                                                                            AASS9515 standard: DNA; 66788 BP
                                               Propionibacterium acnes
                                                                                dermatological; osteopathic; neuroprotectant; ds.
                                                                                                                                                                                                     13-FEB-2002 (first entry)
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#X#X###X#X#X#X###X#X###X#X###X#X###X#X###X#X####X#X###
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Db. [908] Tadaqaccacaccqaqqa 19098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the sample. The polypeptides may be used as antiques in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downrequiate expression and activity of P. acnes polypeptides and therefore treat P. acnes intections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immentosorbent assay (ELISA). This sequence encodes the polypeptides shown in AAU4181 42019 and AAU67474.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07 JUL 2000; 2009US:216747P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis of medical conditions caused by P. acnes. The disorders include SADHO syndrome (Synovitis, acros, pustiolsis, byperforts and esteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne is particularly involved in the inflammatory lesions associated with acne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium aches polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L'maisonneuve J. Zhang Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky YAW, Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CORI ) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 APR 2001; 2001WO US12865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vulgaris. A method for detecting the presence or absence of P. across in a parient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Propionihaeterium acnes immunojenie polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 10; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating aene vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 APR 2000; 2000US 199047P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAS59506 AAS59804 represent DNA molecules encoding
                                                                                 identification; cytostatic, cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; qynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; que therapy; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 66788 BP; 13534 A; 21369 C; 19347 G; 12530 T; 8 other;
                                                              neural disorder; immune system disorder; muscular disorder;
                                                                                                                                                                                                     Human colon cancer antigen nucleotide sequence SEQ ID No.236.
                                                                                                                                                                                                                                                                                                                                         AAC98226 standard; cDNA; 683 BP
                intections disease; cardiovascular disorder;
                                    reproductive disorder; gastrointestinal disorder; renal disorder;
                                                                                                                                                         Human; eolon cancer; colon cancer antique; diagnosis; detection;
                                                                                                                                                                                                                                                  09 MAR 2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16.4; DR 23; Length 66788; Prod. No. 1.80(02); 0; Mismatches 1; Indols 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carter b;
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Job time:

22622 sec

Search completed: September 20, 2002, 10:47:58

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Mat ches
                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                             chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, mascular disorders, reproductive disorders, qustrointestinal disorders, wounds, renal disorders, intections diseases, and cardiovascular disorders. AAC98764 to AAC9872 and AAR54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₩0200055351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                              proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for
                                                                                                                                                                                                                                                                                                                                                                                                     neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiintective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colon cancer associated dene sequences, referred to as colon cancer antiques, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 · MAR - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08 MAR-2000; 2000WO US05883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 called human colon cancer antiques, given in AAB53234 to AAB54006. The human colon cancer antiques can have cytostatic, cardioactive, muscular:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 657; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC97991 to AAC98763 encode the human colon cancer associated proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders such as colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 SEP 2000
                                                                                                                                                                          Sequence 683 BP; 143 A; 210 C; 184 G; 136 T; 10 other;
                                    l ggetaaagaeeteaeegagga 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-587534/55.
ggetgaaggeettaeegagga 295
                    18;
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9905-0124270
                                                                                                77.1%; Score 16.2; DB 21
85.7%; Pred. No. 1.6e+02;
                                                                                                                  Score 16.2; DB 21; Length 683;
                                                                                  Mismatches
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